GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

nucleic search, using sw model oreleic Mc

Run on:

Auqust R 2001 18-25-ff ; Grarch time :=2 Ff Scrouds (Without alignments) 3752.04: Million cell apdates/sec

US 99 475 794 4 1509 Title: Perfect score:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

730101 seqs, 313950809 residues Sear ched:

lotal number of hits safistying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2690999000

Post-processing: Minimum Match 0%

Listing first 45 summaries Maximum Mateh 1908

Database :

N_Geneseq_0601:• 1: /cgn1_9/geqdata/geneseq/geneseqp/NA1980_FAT+• 2: /cgn1_a/gedata/geneseq/geneseqp/NA1981.6A1.• 3: /cgn1_9/gedata/geneseq/geneseqf.com36b.tbA1.•

/cqnl_9/qcqdata/qeneseq/qeneseqn/NA2001.DAT:* Angual 975 godata/geneses/depassagu/NA2600 LAT

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB 1D Description			æ				
100.0 1509 21 AAA51610 84.6 1479 21 AAA51626 84.6 1479 21 AAA51625 79.6 1515 21 AAA70412 79.6 4512 21 AAA70472 79.6 4689 21 AAA70471 79.6 4766 21 AAA70475 79.5 2031 21 AAA70415 79.5 2031 21 AAA70415	Kesult No.			Length	E B	1D	Description
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1117.8	1117.8	1117.8	1077.4	1077.4	1049-2	971.4	9.69.8	930.2	940.2	930.2	925.4	925.4	#1605	916.6	734.2	300.6	704.6	9.899	654	651.8	646	642.2	642.2	642.2	642.2	642.2	642.2	642.2	642.2	642 2	51.5	542.2	562.2
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ALIGNMENTS

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AAASI610 standard: DNA: 1509 BP.
                                                            AAA51610;
                AAA51610
RESULT
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(first entry) 11 1. 2000 HIV synthetic Gag polynucleotide.

The cypression crossette, attiquate, type ${\mathbb Q}_{\ell}$ HIV, Enc. synthetic, in a longestion, packaging cell line, antique presentation; ss.

Human immunodeficiency virus type C strain AF110967. Synthetic.

W0200019304-A2.

06-JUL-2000.

99WO-US31273. 30-DEC-1999;

980\$-0114495. 9908-0152195. 31-DEC-1998; 01-SEP-1999;

(CHIR) CHIRON CORP.

Barnett S, Zur Megede J;

WP1: 2000-452401/39.

Polynucleotide encoding antiquate type C HIV Gag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV

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                                                                                                                                                                                                                 production of Gay- and/or Euv-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or
                                                                                                  Expression cassettes comprising a polynuclectide encoding antigenic type C human immunodeficiency virus (HIV) Gag or Env polypeptides are useful in DNA immunication, generation of packaging cell lines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540
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                                    Claim 2; Page 93; 113pp; English.
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                                                                                                                                                781 eggtggateateetegggeetgaaeaagategtgeggatgtanagenngtgageatertg
                                                      841 garaturgecoqqqeereaagqaqeertleeqeqaartaeqtqqaeeqetfottoaaqaee
                                                                                             841 gacatengeragggennaaggagnenttergegaantangfggaengettettraagaen
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DNA immunization; packaging cell line; antigen presentation; ss.
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1201 Egengnyenennengaagaagayet getagaagt ynggeaaygagggeannagat gaag (1260) 1201 tgeegegeeeeevyvacaayaayyvityeityyaaytaryveiagyaayageeastayaag 1260 1261 gaetgeänegagegeenaggeenuetfeetgggenaagatetggeeneageeneauggeene 1320 1321 conggraactioniycagaachdnaqegaqoroqeeqeeqeeqitqeecacgeeeer 1380 1441 cacqaqeeetaveeqeqaqeeetqaeeqeeetavaqeaqeetutteqqeaqeqqeeeetq 1500 102] gaqqaqatqatqaccqcctqccaqqqcqtqqqqqqqqccqqqccacaaqqqccqqqtqctq 1080 geogaggeoatgagoomaggeomaacagegtgaacutoatgatgatgcagaagagomacttoaag 1140 1141 gacceerggegeaacuteaagtgetteaaetureuraugaugaugeeategeaagade 1200 1381 cocqeeqaqacticeqoticqaqqaqaccaeeeeeeeeeeeaaqcaqqaqeeeaaqaae 1446 961 I kagaas quedaam wegaad quadaga kat set gegasy 13 15 squees quegestade (q. 1020 96] caqaacqecaaceceqactgcadqaccatectgcqcqccctqqqpcccqqcgccacctq 1020 661 gecoregareagat gegegeeereeggaraaraayayaaaat egeeggaggeaceageaeet g 720 661. appopipagnoaapalandogabhningkanganaan aanathan naganghnan aasaahni 920 781 egetggateateetgggeetgaaeaaqateg1geqeatgtaeaqeeeeqtgageateetg 840 841 gabatengenagggenebaaggagenettengengastangtggaengenttetteaaggaen 900 901 ctgegegegaagaayeeaaneraagaacqtgaaatgaactgaatgacqaaqaeeqaaqaeettuetqqtq 960 etgegegegagageeaeeeaggaangtgaagtaaactggutganegagaaneetgetggtg 960 601. accaticaacgangangnngmi qaafiqqqaii ayntadan i iytaraya aqay qay i noqta. 660 601-accateaacqaqqaqqeegeeqeqqqqqeeqeetqeeeeeegqtqeaqqeeqqeeqtq-660 781 eqqtigaalcatestqaqqeetqaacaaqaleqtacqqatqtaeaaqeeeqtqaqeateetq AAA51609 standard; DNA; 1479 RP. 31-OCT-2000 (first entry) 1501 agecagtaa 1509 1501 agecaqtaa 1509 AAA51609; 1081 1081 RESULT AAA51609 $\frac{1}{2}$ qq 9 ζ <u>q</u> Š OYqq 22 QC $\overset{\circ}{\circ}$ $\stackrel{>}{\sim}$ 3 \bigcirc qq Qγ õ òγ Š ò $\dot{\Omega}$ ò ò

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                                                                                                                                                                                                                                                                "Codon usage pattern was modified and inhibitor; elements (INS) and RRE sites were inactivated resulting in improved expression"
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                                     Gag; expression cassette; antiquaic, type C, HIV, Env; synthetic; DNA immunization; packaging cell line; antiqua presentation; ss
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                                                                                                            Human immunodeficiency virus type C strain AF110965.
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                                                                                                                                                                                   Location/Qualifiers
HIV synthetic Gag polynucleotide
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production of Gaq and/or Env-containing profeins. Synthetic Env and Gag expression classettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into non-infectious virusalike particles which are used as
                                           1978 enemerandadadettendettegagagagagagenenggenenaggagagenengad
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1138 aaqageeeeegeetegtgaaqtgetteaactycggeaayyayyyeeaestegeeege 1197
                                                                1198 aactgeegegeeeeegeaagaaggetgetggaagtgeggeaaggagggeeaceeeagatg 1257
                                                                                                                                 1198 aactgeeyeyeeeeegeaayaayyyetgetgyaaytyeyysaayyayyyeeeyyseyyy
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                                                                                                                                                                                                                                  Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV-1; AIDS; Gay; vaccine, expression cassette, as.
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The present sequence is the coding sequence of a HIV Gag expression cassette, Gag.M.dSF2. The Gag priving of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV

Claim 3; Fig 7; 391pp; English.

infection and acquired immunodeliciency syndiume (Albs).

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(By M. Walker C.
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88.5%; Pred. No. 7e-142;
tive 6; Mismatches 140; indels 36;
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Claim 21; Fiq 63; 391pp; English.
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3659 arrannagnanntgnaggagnagaleggetggatgaecaacaacaccecccateccqtq 3718
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3719 ggcgagatetacaagggtggateateetggggeetgaacaagateytyeygatgtacage 3778
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                                                                                                                                                                                                                                                                         HIV bicistronic construct gp160.modSF162.dr1V2.Gag.modSF2
                                                                                                                                                                                                                    HIV-1; AIDS; Gag; vaccine; expression cassette; Env;
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The present invention relates to synthetic HIV Gag and Env expression cassettes. The Gay protein of HIV is needed for the assembly of virus-like particles. In addition, the Gay protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post entry steps in viral replication. The expression cassettes may be used for the recombinant expression of HIV Gag- and Env-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS). The present sequence is a synthetic construct constructed in the generation of the expression rassettes of the present invention. This construct is bicistronic in that the coding sequences for Env and Gag are under the control of a single CMV promoter and between the two coding sequences an internal Ribosome Entry Site (IRES) is present.
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                                                                                                                                                            Barnett S, Zur Megede J, Srivastava I, Lian Y, Hartog K,
Greer C, Selby M, Walker C;
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The present invention relates to synthetic HIV Gaq and Env expression cassettes. The Gaq protein of HIV is needed for the assembly of virus-like particles. In addition, the Gaq protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post entry steps in viral replication. The expression cassettes may be used for the recombinant expression of HIV Gaq- and Env-polypeptides which may then be used to vaccinate against HIV
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                                                                                                            AAA70471 standard; DNA; 4689 BP
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Matches 1351; Conservative
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                                                                                                                                                                                                                                  AAA70471;
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RESULT
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3336-ct ggggceagc tycaycocayoot goadacougoaqoyaaqaqdi qoqaqootgtacaac-3395

300	34	25	40 35	q 465 g 3635	52 36	9 58 y 37	g 64 g 38	Ć 80		c 825 - 399	ა 88 - ი - ი	945 411	7 10 – 10 – 10 – 10 – 10 – 10 – 10 – 10	106 423	C∔ Œ	118 435	2 4	g 130
aggteegegaeaecaaggagg	acgtcaaggacaccaaggagg adaagccaccaaggagg	agaaggcccagcaggrogrog	actacccatcgtgrag 	cctgaacgcctgggtgaagg 	cegeeetga gegeeetga	gtgggeggeeaee 	gagtgggaccgcctg 	cqcqqcaqcqacatcqccg 	accadeacececetteeeg	aacaagat aacaagat	gagecetteeqeyactacyty 	naqqacqtqaaqaactq 	ccatectyegegorotoro 	sagggegtqqqeggg 	.ccaacuqcqtqaacatcatg 	aagtgette aagtgette	aagggetg aagggetg	gggcaagatc
cacctgtactgcgtgcacgccggcatc		igaycagaacaagt 	gear ranga 	agatggtqcaccaggccalcagc 	agaaggcctcagcccgaggtgatccco 	cccaygacotgaacacgatgttgaacaco 	qacaccatcaacgaggaggccgcc 	cerrytggrerenggecagatgegegae 	gcarritgraggagragategretggate 	ctacaagegglggaleateetgggeelg 	gacatecgecagggeeeeaag 	nngageaggenaec 	tyctygtgragaarqecaaceegaetg 	gocacootggaggagutgalgaongootg 	ngcytyctygengaganatuadeea 	agcaacttcaagggrereeggegeaeg 	atogocaagaactgocgogocococyca 	caccagatgaaggactgcaccgagcgcca
11 accqtg		01 ctggaca 56 ctygaga	61 geega 16 geege	06 cagggc 	66 atega 11 36 gtgga	26 gecaee 	86 cagatg 	46 cagace 16 cacgee	Úb gecace IIIII 76 aceaeo	66 qgcgac 	26 ecegtga 96 eeeaee	86 egette 	46 gagaee 16 gagaee	00 90 11 20 90	= 60 − 20 20 − 20	23 cagaa 96 cageg	183 ggcca 356 ggcca	243 gaqgg
2y 24	33	OY 34.	Qy 3	Qy 4 Db 35	Qy 4 Db 36	uy 5 ub 36	Qy 5 Db 37	m	·	Qy 7			4	-1	F4 ** *	ন †	1 4	

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The present invention relates to synthetic HIV Gay and Env expression cassettes. The Gag protein of HIV is needed for the assembly of stages. The Gag protein is needed for the assembly of stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassettes may be used for the recombinant expression of HIV Gag- and Env-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS). The present sequence is a synthetic construct constructed in the generation of the expression cassettes of the present invention. This construct is bicistronic in that the coding sequences for Env and Gag are under the control of a single CMV promoter and between the two coding sequences an internal Ribosome Entry Site (IRES) is present.
                                                              4578 agecagaageaggageceategacaaggagetgtaceeeetgaeeageetgegeageetg 4637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression cassettes encoding the human immunodeficiency virus (HIV) gaq-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Zur Megède J, Srivastava I, Lian Y, Hartog K, Liu H; Selby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4766 BP; 1051 A; 1638 C; 1409 G; 668 L; 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV-1; AIDS; Gag; vaccine; expression cassette; Env; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                 HIV bicistronic construct gp160.modUS4.Gag.modSF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Human inmanodeficiency virus type 1.
                                                                                                                                                                                                    4638 tteggeaacgaeceeageageeagtaa 4664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; Fig 61; 391pp; English.
                                                                                                                                                                                                                                                                                                                     AAA70470 standard; DNA; 4766 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0168471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Cytomegalovirus
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                                                                                                                                                                                                                                                                                          RESULT
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Score 1201; DB 21; Length 4765; Pred. No. 6.9e-142;

79.68; 88.58;

Query Match Best Local Similarity

Matches	0; Mismatches 140; Indels 36; Gap	
	l atgggegeregegerateetgegeggeggegaenetggaeaagtggaeaagtgggaeagateege 60 	
61 293	. etgegeeeggeggaagaagaactacatgetgaageacetggtgtgggeeageegag 120 	
	igeetaetagagaeegeegaggeetgeaged 	
181 413	atqaaqcaqctqcaqccctqcaqaccqqcacqqqqagqtgcqqcctqtacaac 240 	
241	accytytyceaeectytaitycytycacyceygeategayteegeyaeaeeaaygagee 300 	
1 04	ctiquacaaqatiqaqqaqqaqqaqqaqqaqteecaqeaqaaqaeecaqeaqqeeaqaqagagi 360 -	
46.1 19.4	gergaegaea	
406 653	- cagggeragatggggereaggereateagereregeaerertgaaegertgggggaaggtg 465 (BHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	
466		
526	<u> </u>	
586 833		
648 893	- naggerggeeretggeerereggeeagalgegrgaeneegeggeageggeagegge 705 	
706 953	o genaricagnacynt gnaggagnagat ngoch gyat gannagnaan cheener t genegt g. 765 	
76.6. 0.1.3	- ggogagatotacaagogatgaalcatcotaggootgaacaagalogtgoggatgtacagc 825 	
826 073	o cecytyaycaicetygaeatecycagggeeecaaggaeetiin gaeatacyfgae 885 	
886 4133	s eqriticiticadga collacycac gagcaga cacceaggacytgaagaactgaatgace 945 	
946 193	- gagaeretgetggtgeagaegeeääeeeegaetgéaagaeateetgegeeletegge 1005 	
900	o cheqqeqeactet qqaqqaqatgatqaceqeet qeeaqqqeqtqqqeqqeecqqqeeae 1065 	

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4373 cagegegeaact.teegeaaceagegaageggaagegfeaagtgeffeaagtgeggeaaggag 4432
                                                                                                     1183 ggecacategecaagaactgeogreeeeeegaaagagatgeaagtgeagtgeaag 1242
                                                                                                                                                                                                             1303 eccagedacacaaqqqeeqeneeqqeaaetteetgeaqaaneqqaaqeqaqeeqeeqeeere 1362
                                                                                                                                                                                                                          1363 accqtqcgcaccqccqccqccqaqaqcttccqcttcqaqqaqaccaccccqcccc 1422
                                                                                                                                                                                                                                                                               cradedqqqtqaacatedqatq 1122
                                                                                                                                                                                                                                                                                                                                                 4655 agecagaaqcaqgaqcccatcqacaaqqaqctqtaccccrtqaccaqcctqcqcaqcctq 4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a HIV dag/Hepatitis C virus (HCV) core tusion coding sequence. The Gag protein of HIV is needed for the assembly of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV-1: Albs: Gag: vaccine; expression cassette; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic HIV Gag/HCV core insion coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Pages 341-342; 391pp; English.
1066 aaqqoonqoqtqotqqqqqqqqqqqqqq
                                                                                                                                                                                                                                                                                                                                                                          1483 tinggradengereectgageragtaa 1509
                                                                                                                                                                                                                                                                                                                                                                                      4715 tteggeaegaeeeeageageagtaa 4741
                                                                                                                                                                                                                                                                                                                                                                                     AAA70415 standard; DNA; 2041 BP
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99US-0168471.
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present sequence was cloned and used to generate the explession cassettes of the present invention. The expression cassettes may be used for the recombinant expression of HIV Gaq-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome stages of the HIV life cycle, including assembly, virion maturation after particle release and early post entry steps in viral replication. The present invention relates to synthetic HIV Gag expression cassettes. The virus-like particles. In addition, the Gag protein is involved in Many

cagaigcigaaggacaccaicaacgaggacggccgagigggacgccgccgcgig 645 cagatgetgaaggagaceateaaegaggaggeegeegagtgggaeegegtgeammyld 666 gecaccageacectgeaggageagategeetggatgaecageacecececegtgeegtg 765 67 etgegeeceggeggeaagaagaagtacaagetgaageacategtgtgggeeageegeg 126 121 etggagggettegeeetgaaceeeggeetgetggagarngrngaggggtggaagate 180 241 accgiggccacccigiaeigcgigcacgccggcaingaggiccgcgacaccaaggaggcc 300 accgtggccaccctgtactgcytgcaccagcgcatcgacgtcaaggacaccaaggaggcc 306 ctggacaagategaggaggageagaacaagteecageagaegeeceageegeageeaggag 360 ctygagaagategaggaggageagaacaagteeããgaagaagaeeageaggeegeegee 366 geogaeggeaadgtgagecagaactacceratrgfgragaantg 405 geogeoggeacegycaacageagocaggtgagecagaactaceccategtgeagaacetg 426 cagggecagatggtgcaccaggccatcagccccggcacctgaacgcctgggtgaaggtg 465 cagggccagatggtgcaccaggccatcagcnnncgnannigaangnntgggtgaaggtg 486 ategaggagaaggeetteageeeegaggtgateeeeatgtteaeegeeetgagegaggge 525 paggiriggirinigt gginninggannagat gogogaeceeegeggeageggaeategeegge 705 61 cigogoconggraagaagcactacatgotgaagcacotggtgtgggccagccgcgag 120 127 etggagegettegeegtgaaeeeeggeetgetggagaeeeagegagggetgeegeeagate 186 9 7 atgggegeeegegeeagegtgetgageggeggeggetggacaagtgggagaagateege 66 Caps atgaagcaqctycaycccyccctgcayaddggcaccyaygagrtgrgragrctgtacaac 1 atggggrgrmgrgmagratimtgrgrggrgagaagrtggaraaataqaaaaaatecac 79.5%; Score 1199; DB 21; Fength 2031; 88.5%; Fred. No. 1.4± 141, tive 0; Mismatches 140; Indels 36; Sequence 2031 BP, 4±1 A, 767 C, 646 G, 257 F, 0 other; Matches 1349; Conservative Query Match Best Local Similarity (AIDS). 367 466 487 525 586 607 301 307 406 361 qq δλ рþ οy q Qγ qq qq Ωp qq Š Ob QY Db ΟŸ òγ qq ÓΫ́ οÿ οy Пр δ q ΟŞ Ωp 9. 10.

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1207 ggccacaccyccaggaactgccgcgcccccgcaagaagggctgctgcggcggcggc 1255
                                                                                                                                                                                                                                                                                                                                                     1267 gagggccaccagatgaaggactgcaccgagcgccaggccaacttcctgggcaagatctgg 1326
                                                                                                                                                                                                                                                                                                                                                                                                      1369 eccgageceacegecececegaggagagetteegetteggegaggaggaggaggaeeeeeee 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1423 aagcaggagcccaagganngngagnnrianngngagcnnrigaccgccctgcgcagcctg 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1087 aaggeeegegtgetggeegaaggegatgageeaggtgaegaaeeeggegaeeateatgatg 1146
                                                                                                                                                                                                                                                     1123 cagaayaycaacttcaayggcccccqqcqcqcqtcaaqtgcttcaactgcqqcaaygay 1182
                                                                                                                                                                                                                                                                  ggecacategecaagaaetgeegeegeeeegeaagaagggetgetggaagtgeggeaag 1242
                                                                                                                                                   gagaccetyctygtgeagaacyceaaceeegaetgeaagaeeateetgegegetetegge 1005
                                                                                                                cccgtgagcatcctggacatccgrraqugrrrraaggagrrritrogcgartarqiqqar 885
                         847 occaecageutectggaeateegeeagggeeecaaggageerttongngantaeqtggae 906
                                                  HIV Gay-protedse expression cassette coding sequence GagProt.ModS
                                                                            907 egettetacaaqaeeetgaryeyetgagaeagaeagcaagaaqtgaagaactggatgacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV-1; AIDS; Gag-protease; vaccine; expression cassette; ss
                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1483 tteggeaqeggeeeectgageeagt 1507
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. . m The present sequence is the coding sequence of a HIV Gag-protease expression cassette, Gagpröt Mods. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is inverted in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunoshiticiency syndrome (AIES). 406 -caqqqccatustava caqqcrateavecqcaccetqaacqcetgqqtqq46561 - ct gegenninggeggeagaageant anat get gaageamet ggt.gt ggeerageegeggegg - 120 12] otggagggettegeertgaageeeggeetgetggagageegeegagggagggaageaggate 180 187 etgggeragetykraykeeagestylayareeggeageggaggagetgeagaae 246 401 et upaca a upa equipa qua gra qua a construcción de construcción d Fill TILLS accepted in a conference of the conference of the second section of the second sec 427 ragggecagatggtgrannaggecateagneeeegnaceetgaacgeetgggtgaaggtg 486 487 intriguidadadquict teageneergaggtgateeecatgt teagegeectgagegagge 546 Latyygoyconcycoagrafeetycgogggagaagotygaaagtygggagaagateege 60 Expression casettes encoding the human immunodativiency virus (HIV) Srivastava I, Lian Y, Hartog K, Liu H, 241 accqtgqccaccctqtactqcqtqcacqccqccatcqaqqtccqqqqacaccaaqqaqqcc 247 arregtygypraerentyt arrtycytygeaeragygolategaegylinaaggaeeeedaaggaggee 127 et ggagegettegeegtgaaceeggeet getggagaeeagegaggetgeeggeeagate 18] atgaagcayetgragereygeeetgragareygeacegaggatgegeageetgtatacaae 307 ict ggagaugat ngaggaggaggaggaggagt.chaagaagauggeegageeggeegee 46] gregacqqearrr ririr aqqtqaqreagaaetareerateqtgeagaaeetg 466 atogaqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq 74.1%; Score 1117.8; DB 21; Length 1853; 85.1%; Pred. No. 1.7e-131; Gaq containing polypeptide useful for vaccinating against HIV intertious and acquired immunodeticiency syndrome (AIDS) -0; Mismatches 192; Indels Sequence 1853 BD; 421 A; 624 C; 580 C; 328 C; 0 ather; Claim 5; Fig 7; 391pp; English. Greer C, Selby M, Walker C; Zar Mestedo D OUSTINATION Best Local Similarity (CHIR.) CHIRON CORP. WPI: 2000-452400/39. Matches 1299; Barnett S, Owery Match 5 $\stackrel{>}{\sim}$ qq 3 3 11 5 3 $\stackrel{\sim}{\sim}$ 3 $\stackrel{>}{>}$ $\frac{1}{2}$ D. = â 9

586-cuqatiget gaaggacaceateaacyaggaggeeggeetggaeeggeetggaeeggeeggeeggtg-645

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HIV Gaq-protease expression cassette coding sequence GagProtMod.SF2(GP1).
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HIV-1: AIDS: Gaq-profease: Vaccine: expression eassette; ss
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The present sequence is the coding sequence of a HIV Gag protease expression cassette, GagProtMod.SF2 (GPI). The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome
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                                                                                                                                                                                                                               Hartog K, Liu H:
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Human immunodeficiency virus type 1
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99US-0168471
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Greer C, S
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406 caqqqqccaqatgqtqcaccaggccatcagcccccgcacctgaacgcctgggtgaaggtg 465 133 rtygagogettogorgtgaaccccggcctgctqdagaccaucquqqqqccqccaqatc 192 241 accgtggccaccctgtactgcgtgcacgccggcatcgaggtccgcgacaccaaggaggcc 300 301 ctagacaagatcgayyagyagcagaacaagtcccagcagaagaccaagaggccaaygag 360 373 geogeoggeaceggeadeageageaggtgageeagaactaceeeategtgeagaactg 432 433 cagggccagatggtgcaccaggccatcagccccgcaccctgaacycctgggtgaaggtg 492 36; Gaps 13 atgggcgcccgcgccaqcqtgctgagcggcggcgayctggacaaytgggagaagatccgc 72 193 ctggggccagctgcagcccagcctgcagaccygcagcgaggaggtgcgcagcctgtacaac Score 1117.8; DB 21; Length 1865; Pred. No. 1.7e 131; 0; Mismatches 192; Indels 36; 0 74.18; 85.18; Conservative mest Local Similarity Matches 1299; Consorv Query Match Best Local S Op qq Ωÿ δ qq 0.7 QQ 0ΩΩ ${\rm Q} Y$ ΩD ο̈́λ 9

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qq	853	ccaccagcatcctggacatccgccagggccccaaggagcccttccgcgactacgtggac 912	C7
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qn	1153	cagegeggeaacticegeaaceageggaagaeegieaagigetivaaetyeyyeaaggag 12	_
Οy	1183	ggecacategecaagaactgeegegeeeeeqqaagagetgetgetggaagtgeagg 120	~
qn	1213	ggccacaccgccaggaactgccgcgccccccqcaagaaggyctyctygcyctycegc 12	r-
QY	1243	gaggocaccagatgaaggactgcaccgagcyccaggccaacttcctgggcaagatctag 13	<u></u>
qa	1273	gaaggacaccaaatgaaagattgcactgagacaggctaattitttagggaagatctgg 13	~
QY	1303	cccagccacaagggccgccccggcaacttcctgcagaaccgcagcgagccgccgcccc 13	9
QU	1333	cettectacaagggaaggecagggaatliteiteagageag	27
ζ	1363	accgigcccaccgcccccccgccqqqqcttccqugqagagccaccgcccc	21
qu	1375	ccagagccaacagccccaccagaagagagttcaggtttggggaggagaaacaactccc 14	~
Oy	1423	aagcaggagcccaaggaccgrgaqrirtarrqrqaaqriritgaccgcctgcgcagcctg 14	<u> </u>
qq	1435	totcagaagcaggagccgatagacaaggaactgtatoctttaacttocotcagatcacto 14	<u>5</u>
ΟY	1483	tteggeagegeeeetqageeaqtaa 1509 	
QQ	1495	ttggcaacgacccctcgtcacagtaa 1521	

sequence 1865 BP, 424 A, 627 C, 583 G, 231 T, 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expression cassettes encoding the human immunodeficiency virus (HIV) day containing polypeptide useful for vaccinating against HIV infectious and acquired immunodeficiency syndrome (AIDS)
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Selby M. Walker C:
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                                      AAA70476 standard; DNA; 1865 BP
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RESULT 13
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1006 reeggegeeracest ggaggagat garegeet gevaaggegt uggeggeeerggeerae - 1065
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                                            766. gadaacalictasaagogalggaticatsiitsigas aagaisigtagaagagalgtasage 825
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                                                                                          313 etggagaagalngaggaggagnagaanaagtenaagaaaaaaggeneaggengengengen 372
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The present sequence is the coding sequence of a HIV Gaq-polymerase expression cassette, GaqPol.ModSF. The Gag protein of HiV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag polypeptides which may then be used to varcinate against HIV infection and acquired immunodeficiency syndrome (AIDS).
                 1423 aagcaggagnecaaaggaaccgngagcentaccgngagnnentganngcnntqnqnaqnetg 1482
                                                                                              1435 tetcagaageaggageegatagaeaaggaaetgtateetttaaetteeeteagateaete 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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elby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                  HIV Gag-polymerase expression cassette coding sequence GagPol.ModSF.
1363 accytycecaecycecececyceyayayettecyettegaggagaecaeceegeeee
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                                                                                 1483 tteggeageggeecettgageeagtaa 1509
                                                                                                                                                    immunodeficiency virus type 1.
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99US-0168471.
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67 etgegeeeeggeggeaagaagaagtacaagetgaageacategtgtgggeeageegegag 126
                                       121 ctggagggcttcgccctgaacccggcctgctggagaccgccgagggctgcaagcagatc 180
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Best Local Similarity Matches 1299; Conserv

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The patent discloses new packaging cell line for producing a viral accessory protein independent lentivirus, preferably human immunodeticiency virus (HIV), derived retroviral vector particles.
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                                                                                 1267 quayqararraawtqaaaqattqractqaqagaraqqctaaftttttaqqqaaqatctqq 1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; gene replacement; vaccine; biochemical reagent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Codon optimised Human immunodeficiency virus gag coding region.
                                                                                                                          "qaq protein"
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12-SEP-1998;
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third retrovital nucleotide sequence comprising a DNA sequence of interest and lentivitus, preterably HIV, cis acting sequences required for packaging, reverse transcription and integration.

The packaging cell lines and viral particles can be used for gene therapy of gene replacement with improved safety. They can also be used in the development and production of varcines and biochemical reagents. The present sequence is a gag coding region of codon optimised HIV gagpol sequence. This sequence is used in the packaging cell line. Godon optimisation results in improved expression of the gagpol protein and reduces the risk of recombination between the transfer
The packaging cell line comprises a mammalian cell, a retroviral DNA comprising a coding sequence for a lentification, preferably HIV, gagpol, where the coding sequence has been mutagenised to improve expression of the viral gagpol proteins, a second retroviral nucleotide sequence comprising the coding sequence for a heterologous envelope protein and a
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0; Mismatches 221; Indels
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

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Folymucleotide encoding antiquate type C BIV Cag polypeptide or a BIV Env polypeptide and the polypeptide aseful for immunizing a mammal especially human against BIV
                                                                                                              Gad, expression cassette; antiqenie; type C; HIV; Env; synthetie;
GAA immunistre, perhaging cell line, autigum presentation, ss.
                                                                                          HIV Gag major homology region nucleotides 844:903.
                       AAA51607 standard; DNA; 60 BP
                                                                                                                                                    Human immunodeficiency virus.
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                                                                   31-OCT-2000 (first entry)
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                                             type c human immunication, generation of packaging cell lines are useful in DNA immunication, generation of packaging cell lines and production of Gag- and/or Env-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytotoxic I-lymphocyte (CTL) responses by DNA immunication. Gag of HIV 1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or associated to the immune system of the host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Codon usage pattern was modified and inhibitory elements (INS) and RRE sites were inactivated resulting in improved expression"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide encoding antigenic type C HIV Gag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV
                                                                                                                                                                                                                                                                                                                    Gaps
                               Expression cassettes comprising a polynucleotide encoding antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gag; expression cassette; antigenic; type C, HIV, Env; synthetic;
DNA immunization; packaging cell line; antigen presentation; ss.
                                                                                                                                                                                                                                                    100.0%; Score 60; DB 21; Length 60; 100.0%; Pred. No. 1.5e-10; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                     Sequence 60 BP; 14 A; 22 C; 15 G; 9 T; 0 other;
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/product= Synthetic_Gag
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  Claim 1; Paye 92; 113pp; English.
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production of Gag- and/or Env-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide encoding antigenic type C HIV Gag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gacatcaagcagggccccaaggagcccttccgcgactacgtggaccgcttcttcaagacc 60
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gag; expression cassette; antiquaic, \mathrm{type}\ \mathrm{C},\ \mathrm{HIV},\ \mathrm{Env},\ \mathrm{synthetic}; DNA immunization; packaging cell line; antiqua presentation, ss.
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                                                                                                                                                                                                                                                                                                                                   Length 1479;
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                                                                                                                                                                                                                                       Segugaise 1479 BP, 325 A, 529 C, 463 G; 162 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type C strain AF110965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV codon-optimized synthetic Gag polynucleotide.
                                                                                                                                                                                                                                                                                                                                   100.0%, Score 60, DB 21, 100.0%; Pred. No. 2.1e-10; tive 0, Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated to the immune system of the host.
                                                                                                                                                                           associated to the immune system of the host.
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                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 103-104; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA51625 standard; DNA; 1479 BP
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                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHIR ) CHIRON CORP.
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production of Gaq- and/or Proventaining proteins. Synthetic Envaridacy expression cassettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DRA immunication. Gag of HIV-1 self-assemble into non-infertious virus-like particles which are used as a matrix for the proper presentation of an antiqen entrapped or associated to the immune system of the host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide encoding antigenic type C HIV Gag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression cassettes comprising a polynucleotide encoding antigenic type C human immunodeficiency virus (HIV) sug or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and
Indels 0; Gaps
                                                                                                                                                                                                                                            Gag, expression cassette, antiquie; type C; HIV; Env; synthetic,
DNA immunization; packaging cell line; antiqen presentation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%; Score 55.2; DB 21; Length 60; 95.0%; Pred. No. 4.9e-09;
                                                                                                                                                                                                                BIV day major homology region nucleofides 841-900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim I; Page 92; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV synthetic dag polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA51610 standard; DNA; 1509 BP
                                                                                                              AAA51608 standard; DNA; 60 BP
                                                                                                                                                                                                                                                                                              Human immunodeticiency virus
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                                                                                                                                                                                 (first entry)
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Matches 57, Conservative
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                                                                                                AAA5.16.08
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Expression cassettes comprising a polynncleotide encoding antigenic type C human immanodeficioney virus (HIV) Gag or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and production of Gag and/or Env-containing proteins. Synthetic Env and dag expression cassettes exhibit increased potency for induction of cytotoxic T lymphocyte (CTL) responses by PNA immunization. Gag of HIV-1 self-assemble into non-infectious virus like particles which are used as a matrix for the proper presentation of an antigen entrapped or
                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide encoding antigenic type C HIV Gag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV
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Gad, expression cassette, antiquais, type C. BiV; Env; synthetic:
                     DNA immunization; packaqing cell line; antigen presentation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.0%; Score 55.2; DB 21; Length 1509;
95.0%; Pred. No. 6.9e-09;
tive 0, Mismatches 3, Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1509 BP; 320 A; 556 C; 472 G; 161 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeticiency virus type C striin AF119967
                                                          Human immunodeficiency virus type C strain AFI10967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV codon-optimized synthetic dag polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated to the immune system of the host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 93; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA51626 standard; DNA; 1509 BP
                                                                                                                                                                                                     99WO-US 1127 1.
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Matches 57, Conservative
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                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP.
                                                                                                                     W0200039304-A2.
                                                                                                                                                                                                  30-DEC-1999;
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                                                                                                                                                             06-JUL-2000,
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                                                                               Synthetic.
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AAA70417
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                                                                                                                                                                                                                                                                        Expression cassettes comprising a polynucleotide encoding antigenic type C human immunodeficiency virus (HIV) Gay or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and production of Gag- and/or Env-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or associated to the immune system of the host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "HIV p55 Gag Major Homology Region protein"
/note= "No stop codon given"
                                                                                                                                               Polynucleotide encoding antiqenic type C HIV Gag polypeptide or a HIV Env polypeptide and the polypeptide useful for immuniting a mammal especially human against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Zur Megede J, Srivastava I, Lian Y, Hartog K, Liu H; Selby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.0%; Score 55.2; UB 21; Length 1509;
95.0%; Fred. No. 6.9e-09;
Live 0, Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1509 BP; 321 A; 559 C; 471 G; 158 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV p55 Gag Major Homology Region coding sequence.
                                                                                                                                                                                                                                         Disclosure: Page 104; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Conservative
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                                                                      Barnett S, Zur Megede
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Best Local Similarity
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                                                                                                            WPI; 2000-452401/39
                          (CHIR ) CHIRON CORP
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The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-ontry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV.
                                                                                                                                                                                          The present invention relates to synthetic HIV Gay expression cassettes. The Gay protein of HIV is needed for the assembly of virus-like particles in addition, the Gay protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gaq-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS). The present sequence is the coding sequence of HIV p55 Gag Major Homology Region. This sequence is located within the F24-CA sequence of Gag. Mutations in this region can severely impair particle production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to synthetic HIV Gag expression cassettes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.3%; Score 53.6; DB 21; Length 60;
ilarity 93.3%; Pred. No. 1.6e-08;
Conservative 0; Mismatches 4. r.2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 60 BP; 13 A; 24 C; 15 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV Gag common region coding sequence.
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                                                                                                                                            Claim 1; Page 345; 391pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA70417 standard, DNA; 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US31245.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-452400/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
Les 56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200039302-A2.
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accessory protein independent fertivites, preferably human immunodeficiency virus (HIV), derived retroviral rector particles. The packaging cell line comprises a mammalian cell, a retroviral DNA comprising a coding sequence for a lentivirus, preferably HIV, gagpol, where the coding sequence has been mutagenised to improve expression of the viral gagpol proteins, a second retroviral nucleotide sequence comprising the coding sequence for a heterologous envelope protein and a
                             sequence is a common region found in Gay coding sequences: Gay protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy or gene replacement with improved safety. They can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        third retrovital nucleotide sequence comprising a DNA sequence of interest and lentivirus, preterably HIV, cis-acting sequences required for packaging, reverse transcription and integration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HHV: dad; parkajing cell line; lentivirus; retrovirul vector particle; pol; gene therapy; gene replacement; vaccine; biochemical reagent;
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                     intection and acquired immunodeficiency syndrome (Albs). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New packaging cell line for producing a viral accessory protein
independent HIV derived retroviral vector particles, useful in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses new packaging ceil line for producing a viral
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                                                                                                                                                                                                                         89.3%; Score 53.6; DH 21; Length 1268; 93.3%; Pred. No. 2.2e-08;
                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                            Sequence 1268 BP: 274 A; 449 C; 411 G; 135 T; 0 other;
                                                                                                                                                                                                                                                           Pred. No. 2.2e-08;
0; Mismatches 4
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/product="qag_profein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA252051 standard; DNA; 1503 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIL.) CHILDRENS MEDICAL CENT
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980S-0100063.
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                                                                                                                                                                                                                                                           Best Local Similarity 93.33
Matches 56; Conservative
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P PSDM: AAY70599
                                                               and Gad-polymerase
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in the development and production of vaccines and biochemical readents. The present sequence is a gas coding region of codon optimised BIV gaspol sequence. This sequence is used in the packaging cell line. Codon optimisation results in improved expression of the gaspol protein and reduces the risk of recombination between the transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the coding sequence of a HIV Gag expression cassette, Gag.ModSF2. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life eyele, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression assecte may be used for the recombinant expression of
                                                                                                                                                                                                                                                                                           850 gadatzeyedayyyi deraaygaysi etti riyegaxi taratiyyax i yetti taxaagado 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV GL4-polypeptides which may then be used to vaccinate against HIV infection and acquired immunedaticioney syndrome (AIDS).
                                                                                                                                                                                                                                                                        1 gacatcaaggaaqqccccaaaqgaqcccttccqcgactacqtqqaccqcttcttcaaqacc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression cassettes exercing the bapain imminished oney virus (HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic HIV Gag expression cassette coding sequence dag.ModSP2.
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                                                                                                                                                                                            89.3%; Score 54.6; DB 21; Length 1503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gag containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficioncy syndrome (AIBS) -
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Jby M, Walker C;
                                                                                                                                                                                                                                   4: Indels
                                                                                                                                    Sequence 1503 BP; 339 A; 530 C; 433 C; 201 T; 0 other;
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                                                                                                                                                                                                                Pred. No. 2.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                           AAA70412 standard; DNA; 1515 BP
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Best Local Similarity 93.33
Matches 56, Conservative
                                                                                                                                                                                                                                  56; Conservative
                                                                                                  vector and gagpol mRNA.
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                                                                                                                                                                                                                Similarity
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Greer C, S
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(CHIR ) CHIRON CORP
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                                      Synthetic.
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                                                                                                                                                                                                                                                                                                                                         Greer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AIDS)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                862 gacatecgocayggececaaggagecetteegegactaegtggaeegettetaeaagaee 921
862 garateegeeagggeeecaaggageeetteegegactactacgegttetacaagace 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expression cassettes encoding the human immunodeficiency virus (HIV) Gaq-containing polypeptide useful for vaccinating against \rm HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu H;
                                                                                                                                                                                                                                                          HIV Gag-protease expression cassette coding sequence GagProf.ModS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.3%; Score 53.6; DB 21; Length 1853; 93.3%; Pred. No. 2.3e-6%; Live 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zur Megede J, Srivastava I, Lian Y, Hartog K,
blby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV-1; AIDS; Gag-protease; vaccine; expression cassette, ss.
                                                                                                                                                                                                                                                                                                    HIV-1; AIDS; Gay-protease; vaccine, expression cassette, ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1853 BF, 421 A, 624 C, 580 G, 228 T, 0 other,
                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA70475 standard; DNA; 1865 BP
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                                                                                                                              AAA70413 standard; DNA; 1853 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 93.39
Matches 56; Conservative
                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP
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                                                                                                                                                                                                                                                                                                                                                                                                               W02000 39 402-A2
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                                                                                                                                                                                                                   28-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                           AAA70413:
                                                                                       RESULT 11
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ID AAA7
XX AC AAA7
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qq Qγ

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HIV Gag-protease expression cassette coding sequence GagProtMod.SF2(GP2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) - \,
                                                                                                                                                                                                                                                                                                                                                                                                    Liu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.3%; Score 53.6; DB 21; Length 1865; 93.3%; Pred. No. 2 38-08;
                                                                                                                                                                                                                                                                                                                                                                                                    Hartog K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV-1; AIDS; Gag-protease; vaccine, expression cassette; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1865 BP, 424 A; 627 C; 583 C; 231 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                   jede J, Srivastava I, Lian Y,
Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0: Mismatches
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Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Fig 69; 39ipp; English.
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Matches 56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-452400/39.
                                                                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                     Selby M,
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The present sequence is the coding sequence of a HIV Cag-protease expression cassette, SagrottotMod.SF2(CF2). The Cag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life eyele, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome.
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                                                                                                                                                 Expression cassettes encoding the human immunodeticiency virus (HIV) Gag containing polypeptide useful for vaccinating against HIV
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  Harrey K. 114 H.
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Selby M, Walker C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.3%; Score 53.6; DB 21; Length 1865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                               infections and acquired immunodeficiency syndrome (AIDS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1865 BP; 460 A; 583 C; 569 G; 253 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV-1: AIDS; Gay; Vaccine; expression cassette; ss.
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     1 13th Y
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Tive 0, Mismatches
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  Crivactava !
                                                                                                                                                                                                                                                                      claim 5; Fig 70; 391pp; English.
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Selby M. Walker C;
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                                                                                          WPI: 2000-452400/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 56, Conserve
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Barnett S.
Greer C. S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (A115)
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The present sequence is the coding sequence of a HIV Gag-polymerase expression cassette, GagPol.ModSF. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion
                                                                                                                                             present sequence was cloned and used to generate the expression cassettes of the present invention. The expression cassettes may be used for the recombinant expression of HIV Gaq-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome
virus-like particles. In addition, the Gaq protein is involved in many stages of the HIV life eyele, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The present invention relates to synthetic HIV Gaq expression cassettes. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53.6, DB 21, Length 2041;
Pred. No. 2.3e-08;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53.6; DB 21; Length 4319;
Pred. No. 2.5e-08;
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                                                                                                                                                                                                                                                                                                                                                               Sequence 2031 BP; 421 A; 707 C; 646 G; 257 T; 0 other;
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Greer C, Selby M, Walker C;
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Search completed. August 8, 2001, 18:24:58 Job time: 12602 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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zur Megede,J., Chen,M.C., Doe,B., Schaefer,M., Greer,C.E.,
Selby,M., Otten,G.R. and Barnett,S.W.
Increased expression and immunogenicity of sequence-modified human immunodeficiency virus type 1 gag gene
J. Virol. 74 (6), 2628-2635 (2000)
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Direct Submission
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Query Match

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/note="derived from Human immunodeficiency virus type lisolate YU-2"
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/dk_xrof="G!:11966867"
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Fuller.M. and Anson, b.S.
Direct Submission
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KVYLAWVPAHKGIGGNEQVDKLVSAGTRKVLFIDGIDKAQEEHEKYHSNWRAMASDFN
LPPVVAKELVASCDKCQLKGFAMHGQVDCSPGIWQLDCTHLFGKVIIJVAVHVASGYTE
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RTRGAHTNDVKOLLEAVÖKTATESTVIWGKTPKFKLPTQKETWETWATEYWQATWIFF
WEFVNTPPLVKLWYQT PKEPLI.GAFTFYVDGAANPETKI.GKAGYVTNKGRGKVVSTTD
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NPQSOGVVESMNKELKKIIGGVREGAEHLKTAVQMAVFIHNFKKKGGIGGYSAGEKIV
DIIATDIQTKELQKQITKIQNFRVYYRDSRDPIWKGPAKLLWKGEGAVVIQDNSDIKV
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/protein_id="AAG28735.1"
/db_xref="G1.11066862"
/translation="MGARASVLSAGPLDKWEK!PIPPGGKK@YPLKHIVWASPFLEPF
AVDPGLLETSEGGRQILGQLQPSLQTGSEELRSLYNTVATLYCVHQKIEVKDTKEALE
                                                                                                                                                                                                                                               YSPTSILDĪRĢGPKEPPRDYVDRFYŘTĪRAEĢASĢEVKNWMTETTLVÓNANPDCKTIL
KALGPAATLBFMMTAPGRYGGPGHKARVLABANSQVTNSATIMMGRGNFRNGRKTVKC
FNCGKEGHIAKNGRAPEKKGGWRGGKEGHGMKF, TERGANFLGKIMPSHKGFFGNFTV
SRPEPTAPSEESVRFGEETTTPSGKÇEFIDKELYPLASLKSLFGSDPSSG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="REDLAFPQGKAPKFSSEQTPANSPIRFF@VWFFINNSLSEAGA
DRQGTVSFSFPQITLWQPPIVTTKTGGQLKFALLIPTGADDTVLFEMNI-PGRWKPKMIG
GTGGFTKVPQYPQTPTETGGHKATGTVLVGPTPVNTTGKNILTGTGCTLNFF1SF1ET
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QYMDDLYVGSDLFIGGHRTRIFELRQHLLRWGFTTPDRKHQKEPPFLWMGYELHFDKW
TVQPIVLPEKDSWTVNDIQKLVGKLNWASQIYAGIKVRQLGKLLRGTKALTEVIPLTE
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KPSTKWPKLVDPPRLNKRTQOFWEVQLGTPHPAGLKKKKSVIVLDVGDAYFSVPLHED
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EKAFSPEVI PMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKET I NEEAAEWDRLHPV
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Submitted (12-JUL 2600) Chamical Patholog,, Women's and Children's
Hospital, 72 King William Road, North Adelaide, SA 5006, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic construct HIV-1-derived gag-pol fusion protein gene,
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90.0%; Pred. No. 4.9e-05;
live 0; Mismatches b;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="pol_protein"
/protein_id="AAG28736.1"
/db_xref="G1:11006863"
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Fuller, M. and Anson, D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fuller, M. and Anson, D.S
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1 (bases 1 to 4353)
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EKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKETTNEEAAEWDRLHPV
HAGPTAPGQMREPRGSDIAGTTSTLQEQTGWMTNNPPIPVGELYKRWITLGLNKTVRM
YSPTSTLDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMTETLLVQNANPDCKTIL
KALGPAATLEEMMTANQGVGGPGHKAPVTAEAMSQVTNSATTMMQFRUFRNGRKTVKC
FNCCKEGHTAKNCRAPSKRGNWRNGKFGHQMKNTTFRQANFLRFDLAFPQGKARKFSS
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PTPVNIIGRNLLTQIGCTLNFPISPIETVPVKLKPGMDGPKVKQWPLTEEKIKALVEI
CTEMEKEGKISKIGPENPYNTPVFAIKKKDSTKWRKLVDFFELNKFTQDFWEVQLGIP
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WCFTTPDKKHQKEPPFLWMGYELHPOKWIVQPIVLPEKDSWIVNDIGKLVGKLNWASO
IYAGIKVRQLCKLIRGTKALTEVIPLTEEAELELABNREILKEPVHGVYYDPSKDLIA
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ALGIIQAQPDKSESELVSQIIEQLIKKEKVYLAWVPAHKGIGGNPQVDKLVSAGIKKV
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AVDDOLLETSEGPP9.11/3QLQPSIAT/SSEET/SSLYNTVATLYCVHQK.EDVKDYKEALE
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PGTWOLDCTHLEGKVILVAVHVASGYIEAEVI PAETGQETAYFLLKLAGRWPVTTIHT
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TAVQMAVEIHNEKPKGIGGYSAGERIVDTIATOIQTKELGKQITKIQNERVYYRDSR
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                              /db_xref="taxon.32630"
/note="derived from Human immunodeficiency virus type l
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Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
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//db xrof="taxon:12721"
x 1214 c 1294 g 685 t
                                                                                                                                                                    /note="codon optimized reading frame"
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                                                                                                                                                                                                                                                               /product="gag-pol fusion protein"
/protein_id="AAG28737.1"
/db_xref="GI:11056865"
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/organism-"synthetic construct"
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Patent: WO 9441397-A 2 19-AUG-1999;
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AX019132
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                                                                                                     isolate YII-2"
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KEYWORDS
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/dote-"qaqpoi>SYNqp- codon optimised qaqpoi sequence"
r 1198 c 1285 g 689 t
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| ETFEL | FLITE FELLE | FLITE FILLE | FLITE FILLE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FLITE | FL
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Score 43: Db 9: Langth 4307;
Pred. No. 0.0066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.7%; Score 43; DB 9; Langth 4307;
83.1%; Pred No 0.0066;
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85.1%; Pred. No. 0.0056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 10; Indels
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                                                            10; indels
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Zdkymet "tawa, 226 kg"
Znote "Codon optimised qaqpol sequence."
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1 (bases 1 to 4307)
Mitropharous, K., Kim, N. H., and Kotsopoulou, E.
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/ordanism "synthetic construct"
                                                                 U; Mismatches
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Patent: Wo 005541-A 2 21-SPP 2009;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2 from Patent WO0055341.
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    (bases 1 to 4307)
ndom, M. and Mitrophanous, K.

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Jordanium "synthetic construct"

Adb_wret="taxon: $26.80"

/note-"pSYNGP5 codon optimised HIV-1 gagpol with leader
sequence from the major splice donor"

a 1196 t 1802 q 700 t
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Patent: WO 0055341 A 14 21-SEP-2000;
UDEN MARK (GB) ; OXFORD BIOMEDICA LTD (GB) ; MITROPHANOUS KYRIACOS
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/db_xrcf ":axon:326.40"
/note-"pSYNGP4 - codon optimised HIV-1 daupol with 20 bp
of the leader sequence of HIV-1, etc"
a 1194 c 1296 q 693 t
1. gadat.dagagagagaga caaaqaaca offici goga, Lacqtqaaca ogctfortoaagago 59. HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HTTLL | HT
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Submitted (27 OCT-1999) Feeters M., Retrovirus, Ird, BP 5045, 34032
Montpellier cedex 1, FRANCE
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UDEN MARK (GB) ; OXFORD BIOMEDICA LID (GB) ; MIIKOPHANGUS KIKIANGS
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/db_xref:"taxon:32630"
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Human immunodeficiency virus type 1 proviral partial gag gene for
P24, isolate 97SE-1189.
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Human immunodeficiency virus type 1
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/translation="Kivrmyspyslldirggfreperdyvdrefrtlraegatodykn
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                /production_id="CABB5B50.1"
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YVDRFFFKTLRAEQSSQEVKSWMTDTLLIQNANPDCKTILKALGSGASLEEMMTACOGV
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HIV-l isolate TZR5090 from Tanzania qaq protein (qaq) qene, partial
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Ponjife, B. Gilbert, P. Chaplin, B., Vannberg, F., Mwakagile, D.,
Msamanga, G., Hunter, D., Fawzi, W. and Essex, M.
Emerging recombinant human immunodeficiency viruses: uneven
representation of the envelope V3 region
AIDS 13 (13), 1613-1621 (1999)
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Renjito,B., Gilbert,P., Chaplin,B., Vannberg,F., Mwakagile,D.,
Fawzi,W. and Essex,M.
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Human immunodeficiency virus type 1
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Pred. No. 0.28;
0; Mismatches 13; Indels 0.
                                                                                                                                                                                                                                                                                                      65.3%; Score 39.2; DB 59; Length 663; 78.3%; Pred. No. 0.13;
Live 0; Mismatches 13; Indels 0;
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/country "Tanzania"
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Heyndrickx, F. Tanssens, W., Zekeng, L., Musenda, F., Anagonou, S., Van der Auwera, G., Coppens, S., Vereecken, K., De Witte, K., Van Rampelbergh, P., Kahindo, M., Morison, L., McCutchan, F.E., Carr, J.K., Albert, J., Essex, M., Goudsmit, J., Asjo, B., Salminen, M., Buye, A., Study Group on Heterogeneity of HIV Epidemics in African Citnes and
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Zdb_xret "G1:6815750"
Zfracslatise: "Gsliskwarestiastvemservstastbederepterer
TLRAEQAFODVRNWMIDTILVONANDSVRTTIRALGAGILEEMMTACOGVGGPGHRA
RVLAEAMSQVNNTNIMMQRSNFKGSKRIVKTENGGREGH"
                                                                                                                                                                            AF184568 424 Lp PNA VR. 30-JAN-2000
HIV I isolate ZMqpi322 115m Cambin pay protein (ama) gene, partial
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Submitted (O8-SEP-1999) Virology Unit, Dept. of Microbiology,
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                          Human immonodeticiency virus type 1.
Human immunodeticiency virus type 1
Viruses; Ketroid viruses; Ketroviridae: Lentivirus; Primate
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J. Virol. 74 (1), 363-470 (2000)
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Search completed: August 8, 2001, 20:00:32 Job time: 18336 sec

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qb_est2;*
qb_est3;*
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          em_esthuml2:*
em_esthuml4:*
                           em_esthum15:*
em_esthum16:*
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em_estrol9:*
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                      em_esthum14:*
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                                                                    em_esthum22:*
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em_estrol2:*
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em_estrol5:*
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gb_est 41:*
qb_est 42:*
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qb_est44:*
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                                                        em_esthum20:
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                                       em_esthum17:
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gb_est110:* gb_est111:* gb_htc:* em_gss_fun:* em_gss_huml:* em_gss_huml:* em_gss_hum2:* em_gss_hum3:* em_gss_hum4:* em_gss_hum6:* em_gss_hum6:* em_gss_hum7:* em_gss_hum7:* em_gss_hum9:* em_gss_hum9:* em_gss_hum9:*	4855 110.33 4855 110.33 4855	ប្លេង លុខ ៤ ១ ១ ១ ៤ ៤ ៤ ៤ ៤ ៤ ៤ ៤ ៤ ៤ ៤ ៤ ៤ ៤ ៤	98839 98833 98833 98833 9883 98833 78833 98833
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pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAKIES

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AW147097 707011F07
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A1586607 486049D10
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T14732 05c04107-12
BE59575 PI1_54_60
BE917843 OV1_7_610
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BC642290 OV1_25_F1
BF657016 OV2_18_B0
BG073239 OV2_28_F0
BC373239 OV2_28_F0
BC37444 PI1_14_C0
BC374684 OV1_37_A0
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AW922389 DC1_18_H0
BE430582 SUN004.E0
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BE918452 OVI_4_A04
BG550542 947077H05
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BG550414 947074F03
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CSSZZE CSSZZE RICO
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BG355028 947035P65
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Spermatophytas Magnoliophytus Liliopsidas Poaless Poaceaes
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AU031268 AU031268.1 G1:3767158
             Description
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1. (bases 1 to 491)
Sasaki,1. and Yamamoto,E.
Rice CDNA from immature leaf including apical meristem
Unpublished (1997)
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BE595775
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BE364444
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Rosallt
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BG517417 560 bp mRNA EST 30-MAR-2001
947062012.yl 947 / 2 week shoot from barkan lab Zea mays cDNA, mRNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .491
/organism-"oryza sativa"
/strain-"Nipponbare"
/db_xtrf "tavan:4530"
/clone "E61244_22"
/rione_lib-"Rice cDNA from immature leaf including apical
meristem"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Foaceae: PACC
clade, Panicoideae, Andropogoneae: Zea.
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Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
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/note-"9rgam: leat; immature leat including apical
meristem (under long day condition)"
a 127 c 137 q 88 t 6 others
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/clone_lib "947 - 2 week shoot from Barkan lab"
/tissue_type "leaf and stem, including leaf base"
/dev_stage "2 week old seedling (4 leaves)"
/lab_host:"Xhl-Blue"
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Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
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Plate: 947062 row: C column: 12.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                    Email, tsasakidabr.attre.qo.jp
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/cultivar:"B73"
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Tel: 0298-38-7441
Fax: 0298-38-7468
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Fax: 650 725 8221
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/db_xref="taxon:4577"
/clone_lib="707 - Mixed adult tissues from Walbot lab (SK
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Spermatophyta, Magnollophyta; Elliopsida, Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
independent recombinant phage. The plants were greenhouse
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/dev_stage="adult"
/lab_host="DH10B"
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DEFINITION FM1_53_H06.g1_A003 Floral-Induced Meristem 1 (FM1) Sorghum
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855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                            Query Match 47.3%; Score 28.4; DB 154;
Best Local Similarity 70.4%; Pred. No. 34;
Matches 38; Conservative 0; Mismatches 16;
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68.4%; Pred. No. 39;
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Email: walbot@stanford.edu
Plate: 707011 row. F column. 07.
Location/Qualifiers
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/ub_airi- __aroun_i__induced Meristem | [FM]]"
/clone_lib="Floral-Induced Meristems, Vector:
/note="Organ: Floral-Induced Meristems, Vector:
/pBluescript II from Lambda Zap II; Site_l: XhOI; Site_2:
/pBluescript II from Lambda Zap II; Site_l: XhOI; Site_2:
/pBluescript II from Lambda Zap II; Site_l: AhOI; Site_2:
/pBluescript II from Lambda Zap II; Site_l: AhOI; Site_2:
/pBluescript II from Lambda Zap II; Clones to be sequenced were prepared by mass excision."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mmpratt@uqa.edu
Sequences have been trimmed to explude PolyA. vertor and regions
below phred quality 16. The threshold for highest quality sequence
                                                                                                                   Sorghum propinguum
Eukaryota, Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta; Maquoliophyta; Liliopsida; Poales; Poaceae: PACC
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                           Cordonnier-Pratt,M -M., Gingle,A., Sudman,M., Marsala,C. and Pratt
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Flant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
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High quality sequence stop: 141
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propinguum cDNA, mRNA sequence.
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Department of Botany
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Unpublished (1993)
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                                                                                                 Sorghum propinguum.
                                                                                                                                                                                                       (bases 1 to 168)
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                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                           SOCOT
                                                                                                                                                                                                                                                                    /clone_lib "Maize Leaf, Stratagene #937005"
/motor "Vector Doi-7AP; Site_l EroPl: Site_2: Xhol; mENA
isolated from illuminated leaves and sheaths of 5 week old
plant. cDNA directionally cloned into vector. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cordonnier-Pratt, M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inote "Organ: 5-day-old dark-grown seedlings; Vector: Lambda Zap; Site_1 Xbol; Site_2 FeoRI; The library was made from poly-A ENA in the cloning vector lambda ZAP II. Clones to be sequenced wore prepared by mass excision."
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Spermatophyta: Magnollophyta; Elliopsida; Poales; Poaceae, PACC
elade; Panicoldeae; Andropogoneae; Sorghum.
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DG1_121_H05.q1_A002 Dark Grown 1 (DG1) Sorghum bicolor CDNA, mRNA
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Plant Sciences Building, Pm. 2501. Athens, SA 20602-7271, USA
Tel: 706-542-1860
Fax: 706-542-1805
               California Śtate University
Dept Biol Sei, California State Univ, Hayward, CA 94542
Tel: 5108853459
Fax: 5168854747
Email: cbaysdor⊸haywīre.csuhayward.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                           46.7%; Score 28; DB 2; Length 216, 66.7%; Pred. No. 40; tive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An ESF database from Sorghum: dark-grown seedlings
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/clone_lib-"Dark Grown 1 (DG1)"
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                                                                                                                                                                                                                                /db_xref="taxon:4577"
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/orqanism "26a mays"
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Department of Botany
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                                                                                                                                                                                                                                                      /clone="csuh00762"
                                                                                                                                                                                                         /strain-"B73"
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BE356040.1 GT:9297597
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Contact: Baysdorter C
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Best Local Similarity 66.7%
Matches 40; Conservative
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                                                                                                                          Seq primer: SK.
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/organism="Sorghum bicolor"
/dr_xrel="Laxon:4558"
/db_xrel="Laxon:4558"
/clone_lib="Ovary 1 (OV1)"
/note-"Organ: Mix of ovaries of varying immature stages
from 8-week-old plants; Vector: pBluescript 11 from Lambda
Zap II; Site_1: Xho1, Site_2. EcoRI; The library was made
from F-:; A FNA in the desiral vector lumbda ZAP II.
Clones to be sequenced were prepared by mass excision."
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1 (bases 1 to 327)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
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An EST database from Sorghum: cvaries of varying immature stages
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486049610.x4 486 - leat primordia cDNA library from Hake lab zea
mays cDNA, mRNA sequence.
                                                                                                                                      0; Gaps
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The University of Georgia
Plant Sciences Building, Rm. 2502, Atlans, GA 20602 7271, USA
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46.7%; Score 28; 3B 166; Length 219;
66.7%; Pred. No. 40;
tive 0; Mismatches 20; Indels (
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High quality sequence stop: 266
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Contact: Cordonnier-Pratt MM
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Fax: 706 542 1805
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  Query Match
Best Local Similarity
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1 (bases 1 to 347)
                                                Eukaryóta, Vilidiplantae, Streptophytu, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales; Poaceae, PACC
clade; Panicoideae; Andropogoneae; Zea.
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AU097510 Rice shoot Oryza sativa cDNA clone S5505, mRNA sequence.
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/clone_llb="48b - leaf primordia cDNA libiary from Hake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="leaf primordia"
/dev_stage="P7-P11 leaf"
/lab_host="E.coli XL1-Blue MFR'"
/note="Organ: shoot; Vector: Lambda zap; Hake lab cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                    Maize ESTs from various cDNA libraries sequenced at Stanford
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Contact Takuji Sasaki
National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                   855 California Ave, Palo Alto, CA 94304, USA Tel. 650 723 2227
Fax: 650 725 8221
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Rice cDNA from etiolated shoot (2000)
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Plate: 486049 row: D column: 10.
Location/Qualifiers
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PROJECT ='RGP'
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
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91 c
                                                                                                                                                                                                                                                      Stanford University
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                                                                                                                                                                         University
Unpublished (1999)
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Fax: 0298-38-7468
                                                                                                                                                                                                                 Contact: Walbot V
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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AU029576 Rice panicle shorter than 3cm Oryza sativa cDNA clone
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DEFINITION C99276 Five panicle at ripening stage Oryza sativa cDNA clone
E10581_62, mRNA sequence.
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Best Local Similarity 66.7%; Pred. No. 43;
Matches 40; Conservative 0; Mismatches 20; Indels
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/dev_stage="shorter than 3cm"
/ncte="organ: panicle" 67 t 1 others
             /strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/^lone="S5505"
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                                                                                                       1 others
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Rice CDNA from panicle
Unpublished (1997)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai,Tsukuba
                                                                    //olone_lib="Rice shoot"
/note="Etiolated shoot (8 days old)"
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/strain="Nipponbare"
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/clone="E31104_62"
/organism="Oryza sativa"
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PROJECT ='RGP'.
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AU029576
AU029576.1 GI:3762824
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Tel: 0298-38-7441
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Spermatophytu: Maqnoffophytu; Tiliopsida, Poales: Poaceae, PACC
elade: Panicoideae, Andropogoneae, Sorghum.
1 (bases 1 to 364)
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below Phred quality 16. The threshold for highest quality sequence
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Plant Sciences Building, Rm. 2502, Athems, GA 36602-7271, USA
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/dev_stage "ripening stage"
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National Institute of Agróbiological Resources
Rice Genome Research Program
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Zstrain "Nipponbare"
Zdb_xret*"taxon:4530"
Zelone-"Bl0581_62"
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Fax: 706 542 1805
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/clone_lib "ovary 1 (ovi)"
/note="Organ: Mix of ovaries of varying immature stages
/note="Organ: Mix of ovaries of varying immature stages
from 8-week-old plants: Vector: pHluescript II from Lambda
Zap II, Site_1: XhoI; Site_2: EcoRI; The library was made
from poly-A RMA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
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clade, Panicoideae, Andropogoneae, Zea.
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Local Similarity 66.7%; Pred. No. 44;
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                       High quality sequence start: 8
High quality sequence stop: 358
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                                                                                                                                                               "taxon,4558"
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                                                                                           Location/Qualifiers
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ph: 904-492-1928, ext. 301
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University of Florida
Seq primer: PolyTMix
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ph: 510-881-3459
                                                                                                                                                               /db_xret
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/note="Vector: ZipLox, Site_1: Sall; Site_2: Not1: ds-cDNA was prepared from oligo-dT selected mPNA by priming with a NotI oligo- dT oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA PolI. Sall adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed. "
98 c 107 g 68 t 2 others
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PI1_54_G06 g1_A002 Pathagen induced 1 (PI1) Sorghum bicolor CDNA,
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/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Fathogen induced 1 (PI1)"
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation:
Vector: pBluescript II from Lambda Zap II; Site_1: Xh
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
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Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
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                                                             E-mail: robferl@nervm nerdc ufl edu
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High quality sequence stop: 329
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Contact: Cordonnier-Pratt MM
Department of Botany
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                                                                                                                                                                                                                                                                                                    /organism="Sea mays"
/strain="W64A2"
                                                                                                                                Seq primer: F21.
Location/Qualifiers
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fax: 904-392-4072
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cultivar) were infected with pathogen (isolate FRM421 of Collectrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host the pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        irom 8-week-old plants; Vector: pBluescript II from Lambda Zap II, Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the clouing vector lambda ZAP II. Clones to be sequenced were prepared by mass exrision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mmpratt@uqa.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantue, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
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/note-"organ: Mix of ovaries of varying immature stages
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Plant Sciences Building, km. 2502, Athens, GA 30602-7271, USA
Tel: 706-542-1860
Fax: 706-542-1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sabs
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: 0 Matches 40; Conservative 0; Mismatches 20; Indels 0; Gaps

Search completed: August 8, 2001, 20:58:57 lob time: 21841 sec



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(without alignments)
163.192 Million cell updates/sec
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Copyright (c) 1993 / 2000 Compugen Ltd.
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/issue_type "leaf and stem, including leaf base"
/dev_stage "2 wrek pld seedling (* leaves)"
/dab_bost "XL Rhue"
/in to " : thm. shoot, Vector. Lambda ZAF (pRlackeright NF.);
Site_!: EccR!; Site_z: Xhol; Directionally cloned using
Stratagene's Unitage XR cENA cloning kit with the 5' end
at the EroRI site. The library represents 8 x 10e5
independent recombinant phage. The plants were greenhouse
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Walbot,V.
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Hest Local Similarity 70.4%; Prod. No. 44;
Matches 38; Conservative 0; Mismatches 16; Indels 0; Gaps
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/tissue_type-"leaf and stem, including leaf base"
/dev_stage-"2 week old seedling (4 leaves)"
/lab_host "XL1-Blue"
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                                    Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94404, USA
Tel: 650 724 2227
Fax: 650 725 8221
Email. walkot stanford.edu
Plate: 947073 row: D column: 08.
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Pax: 650 725 8221
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Plate: 947061 row: G column:
Location/qualifiers
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/cultivar "B73"
/db_mref "taxon:4577"
/olec_11b "447 1 x
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Contact: Walbot V
Unpublished (1999)
                        Confact: Walbot V
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/note="Organ: short; Vector: Lambda ZAP (pBlueScript SK-); Site_1. EcoBi, Site_2: XkoI, Directionally cloned using Stratagene's Unizap XR cDNA cloning kit with the 5' end at the EcoRI site. The library represents 8 x 10e5 independent recombinant phage. The plants were greenhouse
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547074H04.y3 547 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA
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1 (bases 1 to 592)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
             Stratagene's Unizap_XR cDNA cloning kit with the 5' end at the EcoRI site. The library represents 8 x 10c5 independent recombinant phaye. The plants were greenhouse
Site_1' EroRI; Site_2' XhoI; Directionally cloped using
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/cultivar="B73"
/db_xref-"taxon.4577"
/clone_lib="947 - 2 week shoot from Barkan lab"
/tissue_type="leaf and stem, including leaf base"
/dev_stage="2 week old seedling (3 leaves)"
/lab_host="XL1-Blue"
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Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 947074 row: H column
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Matches 38; Conservative
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RESULT

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Triticum aestivum
Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Triticum.
1 (bases 1 to 524)
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Akhunov, E., Andersen, G.B., Chao, S., Chin, A., Choi, D.W., Close, T.J., Dvorak, J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Kianian, P., Laro, G.R., Miller, P., Otto, C., Nyuyen H.T., Pansch, G.J., Soaton, C.L., Simons, K., Tong, J.C. and Zhang, D.
The structure and function of the expressed portion of the wheat genomes - Salt-stressed sheath CDNA library
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WHE2066_BG7_D1428 Wheat salt-stressed sheath cDNA library Triticum
acstirum cDNA clene WHE2066_BG7_D14, mPNA sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
Clade, Fanicoideae, Andrepsycheae, 20a
1. (bases 1 to 585)
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/dev_stage="adult"
/lab_host-"DH10B"
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855 ralifornia Ave, Palo Alto, CA 94304, USA
Tel. 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford edu
Plate, 707011 row, F column: 07
Location/Qualifiers
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Best Local Similarity 68.4%; Pred No 51;
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Unpublished (1999)
Contact: Walbot V
Department of Riological Sciences
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/cultivar="W23"
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                                                mays cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHOOT
                                              US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, eA 94710, USA 1el: $105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukıryıtıs Viridiplantuc: Streptophyta: Embryophyta: Trachecphyta:
Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at the University of California, Riverside (Akhunew, Chin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in J byorak Lab). Total KNA was prepared from sheath tissue, equal quantities of KNA were pooled from the two samples, polyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Znote-"Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: Xhol; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perform Close, Perform, Kinnian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_llb:"Whoat sail-stressed sheath cDNA library"
/fissac_type="Sheath"
/dev_stage "Adult plant"
/lab_host_"E. coli SoLR"
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                                                                                                                                                                                                  Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 29 Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.7%; Score 28; DB 152; Length 524;
66.7%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Indels
                                                                                                                                                                                                                                                                                                                                    /ordanism:"Triticum aestivum"
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Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                           Zoultivar "Chinese Spring"
Zdb_xref:"taxon-4565"
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                                                                                                                                                                                                                                                                            location/Qualifiers
                                                                                                                                                                                 Email: oandersn apw.usda.gev
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                             Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Triticeae; Triticum.
1 (bases 1 to 647)
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Unpublished (2001)
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                                                                                                                                                Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 5105595818
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Best Local Similarity
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JENNAL ...
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                       COMMENT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Eracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCelade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 370)
Cordonnier-Pratt, M.-M., Ginqle, A., Doan, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Close, Fenton) at the University of California,
Riverside, Plasmid DNA preparations and DNA sequencing
were performed in the OD Anderson lab (all other authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIL_54_G06.q1_A002 Pathogen induced 1 (PIL) Sorghum bicolor CDNA, mKNA sequence.
                                                                                                                                                                                                                                                                                                                                                                              Site 1: FrogEL; Site 2: What; Plants were grown in the greenhouse. Spikes at 5, 10 and 15 DAP were harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made, and the chea were in vive excised to give pBluescript phagemids in the LJ close lab (Choi.
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Plant Sciences Puilding, Fm. 2502, Athons, GA 30602-7271, USA
                        Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.
                                                                                                                                                                               /cultivar-"Chinese Spring"
/dt_xref-"Laxon:4565"
/clone "WHE0926_EN1_122"
/clone_lib "Wheat 5-15 DAP spike cDNA library"
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66.7%; Pred. No. 59;
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                                                                                                                                                             /ordanism-"Triticum aestivum"
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                                                                                                                                                                                                                                                                                           /tisspo_typo-"Spike"
/dev_stage="Adult plant"
/lab_host="E, coli Solk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 112
High quality sequence stop: 329
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Contact: Cordonnier-Pratt MM
                                                                                                         gestien/Qualifiers
Email: oandersnapw.usda.gov
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Fax: 706-542-1805
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                                                                                                                                  647
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Best Local Similarity
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Another Torning of Anthropour Intervent of Promother Torning of Anthronose-infected leaves from two-week-old sorghum plants 48 hr after inoculation; Vector: pBluescript II from Lambda Zap II; Site_1. XhoI, Site_2: EcoRI; Two-week-old sorghum plants (BTX 623 cultivar) were infected with pathogen (isolate FRM421 of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptiblity to authrachose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Chars to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-); Site_1: EcoRI; Site_2: XhoI; Directionally cloned using Stratagene's UniZap XR cDNA cloning kit with the 5' end at the EcoRI site. The library represents 8 x 10e5 independent recombinant phage. The plants were greenbises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG462293 372 bp mPNA EST 2^{0.6}MAP-2001 947046F01.y1 947 - 2 week shoot from Barkan lab 2ca mays CDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                    sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryóta, Viridipluntue, Streptophytu, Embryophytu, Trachcophyta,
Spermatophyta, Magnollophyta, Lillopsidu, Poales, Poaceae, PACC
clade, Panicoideae, Andropogoneae, Zca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize ESTs from various cDNA libraries sequenced at Stanford
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/cultivar="B73"
/db_xref="Laxon:4577"
/clone_lib="947 - 2 week shoot from Barkan lab"
/tissue_type="leaf and stem, including leaf base"
/dev_stage="2 week old seedling (3 leaves)"
/lab_host="Xi1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 69.8%; Pred. No. 87;
Matches 37; Conservative 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 gecagggececaaggageeetteegegaactaegtggaeegettetteaagaee 60
/clone_lib="Pathogen induced 1 (PI1)"
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855 California Ave, Palo Alto, CA 94304, USA
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Email: walbot@stanford.edu
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Walbot, V.
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/organism="Sorghum bicolor"
/db_xref="Laxon:4558"
/clone_lib="Pathogen induced 1 (Pil)"
/rote="Organ: Anthracnose-infected leaves from
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda 2ap II; Site_I: XhoI;
Site_2: EcoPI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               grow older (4 weeks or older), plants resume susceptiblity to anthrachose disease. The library was made from poly-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           below Phred quality 16. The threshold for highest quality sequence
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Spermatophyta, Magnollophyta; Elliopsida, Foales: Poareae: PACC
clade: Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                    BE364444 398 bp mRNA EST 20-JUL-2000
PII_14_C08 bl_A002 Pathogen induced 1 (PII) Sorghum bicolor cDNA,
mRNA sequence.
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Sequences have been trimmed to exclude PolyA, vector and regions
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Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
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Flant Sciences Building, Rm. 2502, Athens, GA 30502-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
                                                           Gaps
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Pred. No. 88;
0; Mismatches 16; Indels 0;
                                                        :
C
      DB 154; Length 372;
                                                                                                                                     8 gocagggccccaaggagccrttccgcgactacgtggaccgcttcttcaagacc 60
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                                                           16; Indels
Score 27.4; DB
; Pred. No. 87;
0; Mismatches
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POLYA-No.
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Contact: Cordonnier-Pratt MM
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Best Local Similarity 69.8%;
Matches 37; Conservative
        45.7%;
69.8%;
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Sorghum bicolor
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947021809.yl 947 - 2 week shoot from Barkan lab Rea mays ebna, mRNA
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Spermatophyta: Maquoliophyta; Liliopsida: Poales: Poaceue; PACC
clade: Panicoideue; Ardropogeneae; Zea
l (bases 1 to 408)
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/db_rref."taxon-4577"
/clone_lib="947 - 2 week shoot from Barkan lab"
/tissue_type-"leat and stem, including leaf base"
/dev_stage-"2 week old seedling (3 leaves)"
/lab_host "XLl-Blue"
                 271 GGAGGACHAAGAAGCCCGGCAGGACGCAGGACGCGACGACGACAAGAGC 323
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69.8%; Prod. No. 88;
five U; Mismatches 16; Indels 0;
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8 goodgaggoo caaqaayo citicay gadtacqiqqaaqaan follooticaaganci 60
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                                                                                                                                      E. 7.
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Contact: Walbot V
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res 37, Conservative
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Spermatophyta, Magnoliophyta, Lilliopsida, Poales, Poaceae: PAC
clade, Panicoideae, Andropogoneae, Zea.

    (bases 1 to 455)

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Stanford University
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Fax: 650 725 8221
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Fax: 650 725 8221
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Department of Biological Sciences
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/dev_stage="2 week old seedling (3 leaves)"
/lab_host="XL1-Blue"
/note="Organ: Shoot, Vector: Lambda ZAP (pBlueScript SK-);
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Stratagene's Unizap XR cDNA cloning kit with the 5' end
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Plate: 947017 row: H column: 06.
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Fax: 650 725 8221
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/note="Organ: shoot; Vector: Lambda ZAP (pBlueScript SK-); Site_1: EcoRI; Site_2: XhoI; Directionally cloned using Stratagene's Unizap XR cDNA cloning kit with the 5' end at the EcoRI site. The library represents 8 x 10c5 independent recombinant phage. The plants were greenhouse
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BG316823 470 bp mkNA EST Z6 FEB 2001
947027C02.xi 947 - 2 week shoot from Barkan lab 2ca mays cDNA, mkNA
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/tissue_type="leaf and stem, including leaf base"
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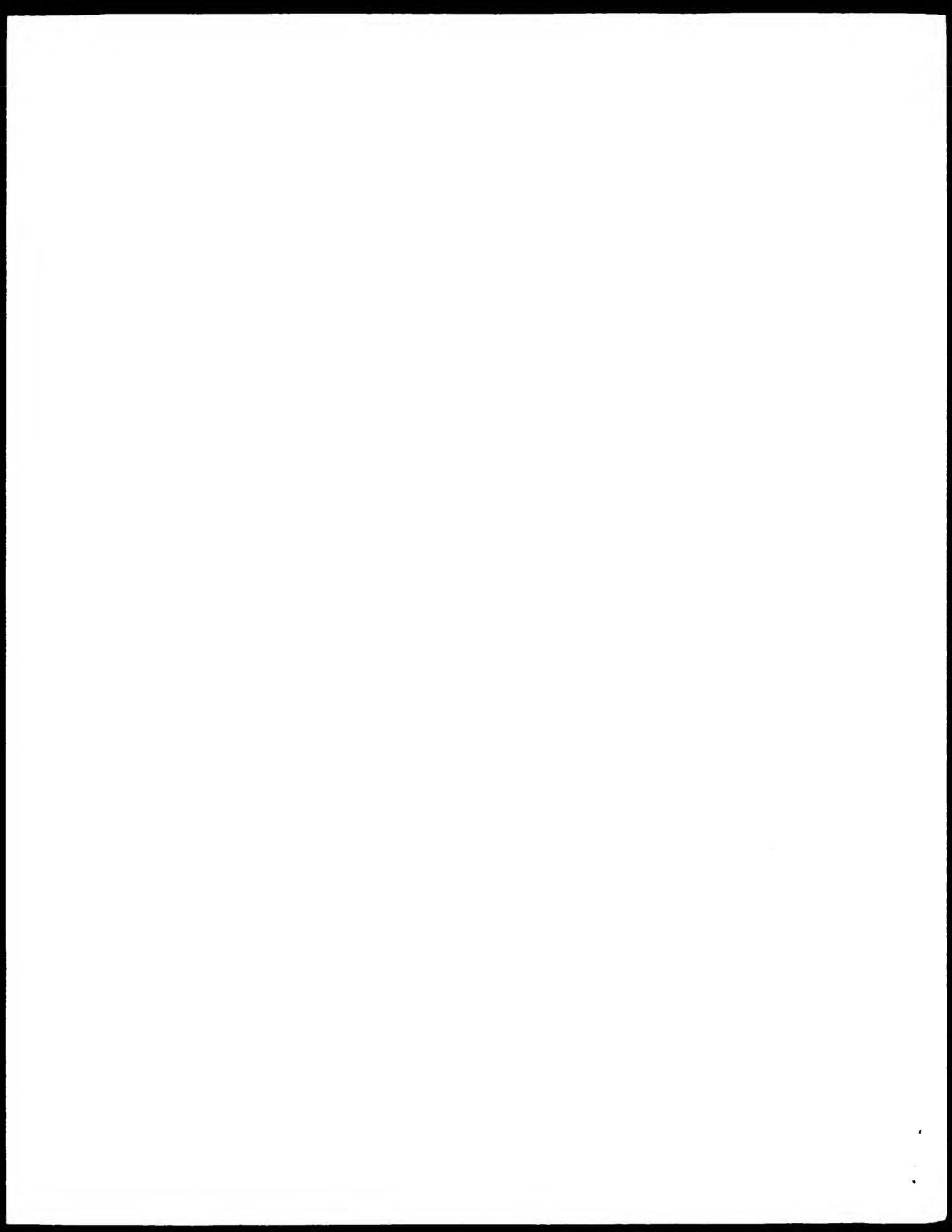
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Zeqn1_37gcddatazgemesegygeneseguzNA1995.DAT;* /cqn1_9/grqdata/geneseq/geneseqn/NA1997_DAF+* /cqii)_9/grqdata/qenesis/genesiqi/NA1999_DAT_* /cqii)_9/grqdata/genesiq/qenesiqi/NA2000_DAT+* N_SCRESCH_9881:*

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SUMMARIES

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ALIGNMENTS

Gad, expression cassette, antiquaic, type C, HIV, Env. synthetic; ENA immunication; packaging cell line; antique presentation; ss. HIV dag major homology region nuclectides 841-900 AAA51608 standard; DNA; 60 BP. Human immunodeficiency virus. (lirst ontry) 31-001-2000 AAA51608; AAA51608 PFSULT

99WO-US31273. 98US-0114495 WO200039304-A2. 30-DEC-1999; 31-DEC-1998; 06-JUL-2000.

Barnett 3, Zur Megede J; (CHIR) CHIRON CORP.

990S-0152195.

01-SEP-1999;

WPI; 2000-452401/39.

Polynucleotide encoding antiquic type C HIV dag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV

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                                    Expression cassettes comprising a polynucleotide encoding antiquence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gag; expression cassette; antigenic, type C; HIV; Env; synthetic; DNA immunization; packaging cell line; antigen presentation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 60; DB 21; Length 60; 100.0%; Pred No 7 20·10; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type C strain AF110967.
                                                                                                                                                                                                                                                                  Sequence 60 BF; 12 A; 24 C; 15 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 93; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV synthetic Gag polynurleotide.
Claim 1: Page 92; 113pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type C strain AF110967.
                                                                                                                                                                                                                                                                                                                                                                                                                     HIV codon-optimized synthetic Gag polynucleotide.
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                                                 0; Mismatches
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                                                                                                                                                                                                                                                                         AAA51626 standard; DNA; 1509 BP
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99US-0152195.
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                                                       hu; Conservative
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       Query Match
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                                                                                                                                                                                                                               "HIV p55 dag Major Homology Region protein"
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Selby M. Walker C:
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                                                                                             HIV-1: AIDS: Gaq; vaccine; expression cassette; ss.
                                                             HIV p55 Gag Major Homology Region coding sequence.
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/note: "No stop codon given"
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                                                                                                                              Human immunodeliciency virus type l.
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Best Local Similarity 98.55,
Test 59, Conservative
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F PSDB; AAB14214.
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AAA70426
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The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life eyele, including assembly, virion maturation after particle release and early post entry steps in viral replication. The expression
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Selby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expression cassettes encoding the human immunodeticiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeticiency syndrome (ALDS) ^\circ
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98.3%; Pred. Ro. 2.7e-09;
tive 6, Mismatches 1, Indels 0;
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                              HIV-1; AIDS: Gaq: varrine: expression rassette: ss.
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/product= "qaq_protein"
                                                                                          Human immunodeficiency virus type 1.
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31-DEC-1998;
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O
                                                                                                                                                                                                                                                                                                                                   comprising the coding sequence for a heterologous envelope protein and a third retroviral nucleotide sequence comprising a DNA sequence of interest and lentivirus, preferably HIV. cis-acting sequences required for packaging, reverse transcription and integration. The packaging real lines and viral particles can be used for gene therapy or gene replacement with improved safety. They can also be used in the development and production of varcines and biochemical reagents. The present sequence is a gag coding region of codon optimised HIV gaypol sequence. This sequence is used in the packaging cell line. Codon optimisation results in improved expression of the gaypol protein and reduces the risk of recombination between the transfer
                                                                                                                                                                                                                                                    The patent discloses new packaging cell line for producing a viral accessory protein independent lentivirus, preferably human immunodeficiency virus (HIV), delived letroviral vector particles. The packaging cell line comprises a mammalian cell, a retroviral DNA comprising a coding sequence for a lentivirus, preferably HIV, gagpol, where the coding sequence has been mutagenised to improve expression of the viral gagpol proteins, a second retroviral nucleotide sequence.
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                                                                                                                                                                           New packaging cell line for producing a viral accessory protein independent \mathtt{HIV} derived retroviral vector particles, useful in genetherapy or gene replacement.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 1503 BP, 339 A, 530 C, 433 G; 201 T; 0 other;
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                                                                         98US-0100063. £ C
                                                            98US-0100022. 60
                                                                                                                                                                                                                                  Claim 41; Fig 8; 62pp; English.
                                                                                                (CHIL-) CHILDRENS MEDICAL CENT.
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                                     99W0-US20675
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               23-MAR-2000
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The present sequence is the coding sequence of a HIV Gag expression cassette, Gag.ModSF2. The Gag protein of HIV is needed for the assembly of virus-like particles, in addition, the Gag protein is involved in main stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome (AIDS).
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                                                                                                                                                  Hartog K, Liu H;
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Selby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.3%; Score 58.4, DB 21; Length 1515; 98.3%; Pt-d N: 2 72-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV-1; AIDS; Gag protease; vaccine; expression cassette; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1515 BF; 329 A; 547 C; 480 G; 159 T; 0 other;
                                                                                                                                                     Barnett S, Zui Meyede J, Srivastava I, Lian Y,
Greer C, Selby M, Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Fig 7; 391pp, English.
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98US-0114495.
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Rest Local Similarity 98.33
Matches 59, Conservative
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                                                                                               (CHIR ) CHIRON CORP.
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(AIDS).
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                                                                                                                                                                                                                                                                              The present sequence is the coding sequence of a HIV Gag protease expression cassette, GagFrot.MedS. The Gag protein of HIV is needed for the assembly of virus like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeliciency syndrome (AIDS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV dag professe expression cassette coding sequence GagProtMod.SF2(GPI).
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Greer C. Seiby M. Walker C.
                                                                                                                                                                                                                                                                                                   97.3%; Score 58.4; DB 21; Length 1853; 98.3%; Pred, No. 2.8e-09; Jee of Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                   Sequence 1853 BP; 421 A; 624 C; 580 G; 228 T; 0 other;
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Claim 5; Fig 7; 491pp; English.
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Matches 59; Conservative
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Greer C. Selby M. Walker C.
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Score 58.4; DB 21; Length 1865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV-1; AIDS; Gag-profedse; vaccine, expression cassette: ss.
                                                                Indels
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                                 Pred. No. 2.80-09;
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                                                              0; Mismatches
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                                                              59; Conservative
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Guery Match
Best Local Similarity
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06-JUL-2000
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                                                          HIV-1; AIDS; Gay; vaccine; expression cassette, as.
                                   Synthetic HIV Gag/HCV core fusion coding sequence.
                                                                              Chimeric - Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                          Example 1; Pages 341·342; 391pp; English.
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                                                                                           Chimeric - Hepatitis C virus.
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Best Local Similarity 48 ..
"ns 59; Conservative
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               28-NOV-2000 (first entry)
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01-DEC-1999;
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The present sequence is the coding sequence of a HIV Gaq-polymerase expression cassette, Gaqpol ModSF. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post ontry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag polypeptides which may then be used to vaccinate agains? HIV intention and adquired immunodeficiency syndrome (AIDS).
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Live 0; Mismatches 1; Indels 0;
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                                                                                                                                                                              Hartog K,
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                                                                                                                                                                          , Zur Megede J, Srivastava I, Lian Y, Selby M, Walker C;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Fig 7; 391pp; English.
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99WO-US31245.
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Lby M, Walker
                                             98US-0114495
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Matches 59; Conservative
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                                                                                                                                 (CHIR ) CHIRON CORP
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30-DEC-1999;
                                                 31-DEC-1998;
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The present ingention relates to egathetic HIV Gag and For expression cassettes. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassettes may be used for the recombinant expression of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gad" and Engrepolypeptides which may then be used to vaccinate against HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection and acquired immunodeficiency syndrome (ADS). The present sequence is a synthetic construct constructed in the generation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression essentes of the present invention, This construct is
Gast containing polypeptide useful for Zaccinating against HIV intections and acquired immunodeticiency syndrome (AIDS)
                                                                                                                                                                        Claim 21: Fiq 64: 391pp: English.
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Sequence 4472 BP; 962 A; 1534 C; 1339 G; 637 T; 0 other;

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                                                                             l qamatimqomaqqqomoqaaqqaqqqottimqqqqamtaqtqqamqottottqaaqaqmi 60
97.3%; Score 58.4; DB 21; Length 4472; 98.3%; Pred. No. 3e-09; tive 6; Mismatches 1; Indels 0;
            Best Local Similarity 98.3
Matches 59, Conservative
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HIV bicistronic construct qp160.modSF162.de1V2.Gag.modSF2. HIV 1; AIDS; Saq; vaccine; expression cassette; Env; ss. Human immunodeficiency virus type 1. AAA70473 standard; DNA; 4608 BP Cytomedalovirus 28 NoV 2000 (first entry) WOZUUU 19 102 - AZ. Chimeric Chimeric AAA70474; FESSEE 1 AAA70474 $\mathbf{X} \times \mathbf{X} \otimes \mathbf{X} \times$

06 JUL 2000.

99WO US ! 1245. 40 DEC 1999; 41 DEC 1998;

9908 0168471. 9805-0114495 DEC 1999;

CHIR) CHIRN CORP.

. Zar Mogede J, Srivastava I, Lian Y, Hartog K, Liu H; Selby M, Walker C; Barnett S. Greer C.

WPI: 2000-452400/49

Expression casestos enviding the boson immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS)

Claim 19: Fiq 64; 391pp; English.

The present invention relates to synthetic BIV Gag and Env expression cassettes. The Gag protein of HIV is needed for the assembly of viras like particles. In addition, the Cag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-outry steps in viral replication. The

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particle release and early post-entry steps in viral replication. The expression eassettes may be used for the recombinant expression of HIV Cag and Env polypeptides which may then be used to vaccinate against HIV
expression cassettes may be used for the recondingnt expression of HIV cag- and Env-polypeptides which may then be used to vaccinate against HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bicistronic in that the coding sequences for Env and Gay are under the control of a single CMV promoter and between the two coding sequences an internal Ribeseme Entry Site (IRES) is present.
                                                                                                 Eleistranic in that the cading sequences for my and day are under the control of a single CMV promoter and between the two coding sequences an
                                      infection and acquired immunodeficiency syndrome (ALDS). The present sequence is a synthetic construct constructed in the generation of the expression cassettes of the present invention. This construct is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection and acquired immunodeficiency syndrome (AIDS). The present sequence is a synthetic construct constructed in the generation of the
                                                                                                                                                                                                                                                                                                                 Expression cassettes encoding the human immunodeficiency virus (HIV) Gaq-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu H;
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                                                                                                                                                                                                                                      97.3%; Score 58.4; DB 21; Length 4608; 98.3%; Pred. No. 30.09;
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Selby M, Walker C;
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                                                                                                                                                                              Sequence 4608 RP: 1001 A; 1589 C; 1382 G; 645 T; 0 other:
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                                                                                                                                        Internal Ribosome Entry Site (IRES) is present.
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Matches 59, Conserva
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Query Match 97.3%; Score 58.4; DB 21; Length 4689; Best Local Similarity 98.3%; Pred. No. 3e-09; Matches 59; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: August 8, 2001, 18:25:01 Job time: 12605 sec

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SUMMARIES

Result		Query	Query	:		
NO.	Score	Match	Length	<u> </u>	II)	Description
1	58.4	58.4 97.3 1509	1509	56	AF201427	AF201927 Synthetic
cı	58.4	97.3	1817	56		AF202464 Synthetic
m	58.4	97.3	1847	56	AF202465	AP202465 Synthetic
4	48.8	81.3	1548	5	AF287354	AF287354 Synthetic
นา	48.8	81.3	4352	ريا (نا	AF287352	AF287352 Synthetic
9	48.8	81.3	4353	56	AF287353	AF287353 Synthetic
7	47.8	7.67	4.307	5	AX019132	AX019142 Sequence
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AF106450 HIV-1 iso
AF106451 HIV-1 iso
AF106453 HIV-1 iso
AF184568 HIV-1 iso
AF250499 HIV-1 iso
                                                                                                                                                                                                                                                             AJ274572 Human imm
L22086 Human immun
AF286235 HIV-1 str
AF319334 HIV-1 iso
AF319347 HIV-1 iso
                                                                            AF110975 HIV-1 iso
AF110975 HIV-1 iso
AJ224196 Human imn
AJ274561 Human imm
AB034321 Human imm
AB034322 Human imm
AB034322 Human imm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  artificial sequence.

1 (bases 1 to 1509)

zur Megede,J., Chen,M.C., Doe,B., Schaefer,M., Greer,C.E.,
Selby,M., Otten,G.R. and Barnett,S.W.
Increased expression and immunogenicity of sequence-modified human immunodeficiency virus type 1 gag gene
I Virol 74 (6), 2628-2635 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (04-NoV-1999) Vaccines, Chilon Corporation, 4560 Horton, Emeryville, CA 94608, USA Location/Qualifiers
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AF286234 HIV-1 str
X52154 Chimpanzee
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U73073 HIV-1 isola
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/db_xref="taxon:32030"
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707 Meyerde, J. and Barnett, S.W.
Direct Submission
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/transl_table=11
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source
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 RESULT
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AVNPGLLETSEGCKÚ LGGLÁPSLQTGSEELRSLYNTVATLYCVHORIDVKDTKEALE
K LEECONKSK K KACKAAAAAGTGNSSÚVSÚNY PLOVNLÓGÁMVHQA ISPRTLNAWVKV
VEEKAFSPEV IPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKET INEEAAEWDRVH
FVHAGPTAPGQMEEPRGSDIAGTTSTLOFQIGWMTNNPPIPVGEIY KPWTILGLNKIV
PMYSPTSTI DIPQGPKEPFPRÝVDPFYKTI.RAEGASGDVKNWMTETLLVQNANPDCKT
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KCENCGKECHTARNCRAPRKKGCWRCGHRGHÇMKTGTERLANTIMMQRGNFRNQRKTV
LQSRPEPTAPPEESFPFGEEKTTPSQKQBPTDKHLYPLTSLRSLFGNDPSSQ"
1 620 c 579 g 228 t
                                                                                          AVNFGLLETSEGCRQTIGGLGFSLQTGSEELKSLYNVATLYCVHQRIDVKDTKEALE
AVNFGLLETSEGCRQTIGGLGFSLQTGSEELKSLYNVATLYCVHQRIDVKDTKEALE
KIEBEQNKSKKKAQQAAAAGTGNSSQVSQVYPLVQHQAMQMLAGINFEATENBWYKV
VEEKAPSPEVIPMSALSECATPODLNTMLNTVGGHQAAMQMLKETINEEAAEWDRVH
PVHAGFIAFGQMREPRGSDIAGTTSTLQEQIGWMTNNPP1PVGEIYKEWILLGINKIV
PMYSPTSILDIPQGPKEPPRYVNPFYKTLPAFQASQUVKNWMTETTLJVQNANPDCKT
ILKALGPAATLEEMMTACQGVGGGHKARVLAEAMSQVTNPATIMMQPGNFPNQPKTV
KCFNCGKEGHTARNCPAPRKKGCWPCGPEGHQMKINTEPQANFIGKIWPSYKGPPGNF
IQSRPFTARPERSPRFGERTTPSQKQEPIDKFLYPLTSLKSLFGNDFSSQ"

543 c 479 g 159 t
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[ (bases 1 to 1847)

2ur Megede, J., Chen, M.C., Doe, B., Schaefer, M., Greer, C.E.,
Selby, M., Otten, G.R. and Barnett, S.W.
Increased expression and immunogenicity of sequence-modified human
immunodeficiency virus type 1 gag gene
J. Virol. 74 (6), 2628-2635 (2000)
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                                                                        /translation="MGARASV|SGGELDKWEKIPLPPGGKKKYKIKHIVWASPELFRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF202464 1847 bp PNA SYN 12-MAP-2000 Synthetic construct gag-protease fusion protein GP1 gene, complete
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For Megede, J. and Barnett, S.W.

Direct Submission

Submitted (05-NOV-1999) Vaccines, Chilom Composation, 4560 Horton Street, Emeryville, CA 94608, USA

Location/Qualifiers
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/db_xret-"GI:7229425"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="synthetic construct"
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/product-"gag protein"
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/db_xref="G1:7248703"
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/transl_table=11
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Score 58.4; DB 56; Length 1847;

97.38;

Query Match

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KTEEEONKSKKKAUUAAAAAGTGNSSQVSUNYFTVQNLQGOMVHQATSPKTLNAMVKV
VEEKAFSPEVTPMFSALSEGATPQDLNTMLNFVGGHQAAMQMLKETTNEEAAEMDRVH
PVHAGPTAFGMPFFPPGSGTAGTTSTLGEGTGWMTNNPFTPVGETYKEMTTLGLNKTV
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/product-"qaq-protease fusion protein GP2"
/protein_id="AAF42820.1"
/db_xret-"G1:7229427"
/franslation="MGAZASVISAGETHEWEFTPIPEDGGETHERVASPETHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMYSPTSTIDTROGPREPFRDYVDEFYRTT.RAEGASGIVKNWMTETLLVÖNANPFORT
TILAATGPAATUEEMMTAUQHVOHTHYRARVTAFAMSQIVTNPAFTMMQHGNE PNQRRTV
ROENGGREGHTARNGBAPEERGOWROGPEGHQMFTNGTEPGANFLORTWPSYRGPPONF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Selby, M., Otton,G.R. and Barnett,S.W.
Increased expression and immunogenicity of sequence-modified haman
immunodeficiency virus type 1 gag gene
1. Virol. 74 (6), 2628-2635 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic construct gad-protease fusion protein GP2 gene, complete
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                                                                                                             LQSPPPTAPPFESPPFGFFWTTPSQRQFPTPKFLYPLTFLPSLPSNDPSSQ"
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98,38; Pred. No. 5.9e-07;
live 0; Mismatches 1; Indels 0;
                                         1; indels
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/db_xref-"taxon:32630"
98.3%; Pred. No. 5.9e-07;
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                                         0; Mismatches
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1 (bases 1 to 1847)
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AVDTOLLET STECKETT GEFORST COMPINE BY I VALIVAT FYNDAEL YN YMER LEAKLERALE.
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Submitted (12 JUL-2000) Themical Pathology, Women's and Children's
Hospital, 72 King William Road, North Adelaide, SA 5006, Australia
                                                                                                                                                                                                                                                                                                                                         Submitted (12-JUL-2000) Chemical Pathology, Women's and Children's Hospital, 72 King William Road, North Adelaide, SA 5006, Australia Location/Qualifiers
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                                                                                                                   Helper plasmids for production of HIV derived vectors Unpublished
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/organism="synthetic construct"
/db_xret "taxon:42630"
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Fuller,M. and Anson,D.S.
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1 (bases 1 to 4352)
Fuller,M. and Anson,D.S.
                                                                                                                                                                                                      2 (bases 1 to 1548)
Fuller, M. and Anson, D.S.
                                1 (bases 1 to 1548)
Fuller, M. and Anson, D.S.
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KVYLAWVPAHKGIGGNEQVDKLVSAGIRKVLFI DGIDKAGFFHFKYHSNWRAMASDFN
LPPVVAKEIVASCDKCQLKGEAMHGQVDCSPGIWQLDCTHLEGKVILVAVHVASGYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEVIPAETGQETAYFLLKLAGRWPVTTIHTDNGSNFTSATVKAACWWAGIKQFFGTPY
NPQSQGVVESMNKELKKIIGQVEDDAEHLKTAVQMAVFTHNFKRRGGIGGYSAGEKIV
DIIATDIQTKELUKQIIKIQNFEVYYRESFI-PUWRGPAKTIMKGBGAVVIQDNSDIKV
VPKKKAKIIRDYGKQMAGDDCVAĞKQUED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEVELEPENDE PROTECTER TRAINETTER TRAINET TEMEKEGKTSKTGPENPYNTPVFAIKK KESTKRERENDE TRAINET FRENTED FILMED TEMEKEGKTSKTGPENPYNTPVFAIKK KESTKREK SVTVLDVGDAYESVPLHED FRKYTAFTIESINNET PGTPYQYNVI. PQCWKGSPAIFQSSMTTILEPFRKONPDLVIY QYMDDLYVGSDLEIGQHRTKIEELRQHLLKWGFT-TPDKKHQKEPPFILWMGYELHPDKWTVQPIVI. PEKDSWTVNDIQKLVGKLNWASQIYAGIKVRQLAKLEKGTKALTEVIPLTE
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RTRGAHTNDVKQLTEAVQKIATESIVIWGKTPKFKLPIQKFTWETWWTEYWQATWIPE
WEFVNTPPLVKLWYQLEKEPIIGAETFYVDGAANREIKLGKAGYVTNKGRQKVVSLTD
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                                                                                                                         /translation="MGARASVLSAGELDKWEKIRLRPGGKKQYRLKH1VWASRELERF
AVDPGLLETSEGGRQ1LGGGGPSLQTGSEELRSLYNTVATLYCVHQK1EVKDTKEALE
                                                                                                                                                                         KIEEEONKSKKKAUOAAADTGNSSOVSONYPIVONLOGGMVHQAISPRTLNAWVKVVE
EKAFSPEVIPMFSALSEGATPODLNIMINTVGGHOAAMOMLKETINEEAAEWDRLHPV
HAGPIAPGOMREPRGSDIAGTTSTLOEOIGWMTNNPPIPVGEIYKRWIILGENKIVRM
                                                                                                                                                                                                                                                                     KALGPAATLEEMMTACQGGGGGGHKARVLAEAMSQVTNSATIMMORGNERNÜRKTVKC
FNCGKEGHLAKNCRAPRKKGCWKGGKFGHQMKD."TERQANFTGKTWPSHKGRPGNFLQ
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                                                                                                                                                                                                                                                 YSPTSILDİRQGPKEPFRDYVDRFYKTLRAEQASOEVKNWMTETLLVQNANPDCKTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"REDLAFPQGKARKFSSEQIFANSFIPFFFGVWFFNNSLSFAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRQCTVSFSFPQITLWQRPI.VTIKIGGQI.KFALLDTGADDTVLEEMNLPGRWKPKMIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIGGFIKVKÝYIV) PIEICCHKAIGTVLVGPTPVNÍIGRNLLÍQIGCÍLNFPISPIET
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                                                                                                                                                                                                                                                                                                                     SRPEPTAPSEESVRFGEETTTPSQKQEPIDKELYPLASLRSLFGSDPSSQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="pol_protein"
/protein_id="AAG28745 l"
/db_xref="G1:11066863"
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Fuller,M and Anson,D.S.
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KALGPAATLEEMMTACQGYGGPGHKARVLAEAMSQVTNSATIMMQRGNFRNQRKTVKC
ENCGKEGHLAKNCPAPPKKGYWKYGKEGHVMKLYTEKQANFLREDLAFPQGKARKFSS
EQTRANSPTRRERQVWRRDNNSLSFAGADKQGTVSFSFFQTTLWQRPTVTKTGGQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EÄLLDTGADDTVLEEMNLPGHWKPKMIGGIGGFIKVRÖYĎGIPIEICGHKAIGTVĽVG
PTPVNIIGRNILTQIGCTLNFPISPIETVPVKLKPGMDGPKVKQWPLIEBKIKALVEI
CTEMEKEGKISKIGPENPYNTPVFAIKKKDSTKWKKLVDFRELNKRTQDFWEVQLGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGSPAIFQSSMTTILEPPRKONPDLVIYOYMDDIYVGSDLEIGGHRIKIĒELROHLIR
WGFTIPDKKHOKEPPFLWMGYELHPDKWTVQPIVLPEKDSWIVNDIQKLVGKLNWASO
IYAGIKVPQLCKLI PGTKALTEVIPLTEEAELELAENKEILKEPVHGVYYDPSKDLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELOKOGOCOMTYOLYOEPFKNLETGKYAPTRGAHTNDVKOLTEAVOKLATESIVIWGK
TPKFKLPLOKETWETWWTEYWQATWIPEWFFVNTPPLVKI.WYOLEKEPIIGAETFYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAGPIAPGOMREPRGSDIAGTTSTLOEQIGWMTNNPPIPVGEIYKRWIILGENKIVRM
YSPISILLDIROGPKEFFFDYVDRFYKTIRAEGASGEVKNWMTETLLVONANPDCKTIL
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TAVQMAVFIHNFKRKGGIGGYSAGERIVDIIATDIQTKELQKQITKIQNFRVYYRDSR
                                                                                                                                                                                                                                                                                                                                                           AVDPGLLETSEGGRO11AQLQPSIQTGSEELRSLYNIVAILYOVHUKIEVKDTKEALE
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                           /db_xref="taxon:32630"
/note="derived from Human immunodeficiency virus type 1
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MITROPHANOUS KYPLACOS (GB); KINGSMAN ALAN JOHN (GB); OXFORD
BIOMEDICA LTD (GB); KIM NARRY (KR)
Location/Qualifiers
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                                                                                                                                              /note="codon optimized reading frame"
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                                                                                                                                                                                                                                       /product="gag-pol fusion protein"
/protein_id="AAG28737.1"
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1 (bases 1 to 4307)
Mitrophanous, K., Kingsman, A.J. and Kim, N.
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Patert: Woodsseal A 2 21 CRF 2000,
Uden mark (GB) : Oxford Blomedica LTD (GB) ; MITROPHANOUS KYRIACOS
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Score 47.8; DB 9; Length 4307;
Pred. No. 0.00045;
0; Mismatches 7; Indels 0;
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88.1%; Pred. No. 0.00045;
tive 0; Mismatches 7; Indels 0;
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Best Local Similarity 88.1%; Pred No 0.00045;
Matches 52; Conservative 0; Mismatches 7; Indels 0;
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/db_xret="taxon,326x6"

/note "Codon optimised gagpol sequence"

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AX056836
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AX045454
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Anti-viral vectors
Patcht: Wo 0055341-A 14 21-SEP-2000;
UDEN MAKK (GB) ; OXFOKD BLOMEDICA LID (GB) ; MITKOPHANOUS KYRIACOS
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/note "psynGP3 - codon optimised HIV-1 gagpol with leader
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7db_arcf "taxon.526.30"

/note "psyNGP4 - codon optimised HIV-1 qaqpol with 20 bp

of the leader sequence of HIV-1, etc"

a 1194 c 1296 q 693 t
1 gacatecquecayyse redanyque etteryoque tarytyque, gettetteuague 59 | HELLILLI (H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H.L. H.H
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88.1%; Pred. No. 0.00045;
tive 0; Mismatches 7; Indels 0;
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/organism-"synthetic construct"
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Patent: WO 0055341-A 13 21-SEP-2000;
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AX035465
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1. .4427
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1 (bases 1 to 4353)
Uden,M. and Mitrophanous,K.
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1 (bases 1 to 4327)
Uden,M. and Mitrophanous,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-NOV-1999) to the DDBJ/EMBL/GenBank databases. Takeshi yamada, Institute of Medical Science, University of Tokyo, Department of Infectious Diseases; 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan (E-mail:take-y@ims.u-tokyo.ac.jp, Tel:81-3-5449-5336, Fax:81-3-5449-5427)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamada.T. and Iwamoto,A. Comparison of proviral accessory genes between long term nonprogressors and progressors of human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                Anti-viral vectors
Fatent. WO 0055341-A 12 21-SEP-2000;
UDEN MARK (GR) ; OXFORD FIOMEDICA LTD (GB) : MITROPHANOUS KYRIACOS
                                                                                                                                                                                                                                                                             /organism="synthetic construct"
/db_xref="taxon:32630"
/note="psyngp2 - codon optimised HIV-1 gagpol with leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1 provinal gene for gag profein p24 region, partial CPS, isolate:patient 5, clone:p24(5)-d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1 (isolate:patient 5) proviral DNA, cloue.524(5).d,p24(5).e,p24(5).i. Human immunodeficiency virus type 1 Viruses; Retroid viruses; Retroviridae, Lentivirus, Frimate
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          15-NOV-2000
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1. .693
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of Virol 145 (5), 1021-1027 (2000)
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             Sequence 12 from Patent WO0055341. AX035463
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/db_xref="taxon:11676"
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                                                                                                                              artificial sequence.
1 (bases 1 to 4642)
Uden,M. and Mitrophanous,K.
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Hest Local Similarity 88.10
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                                                                                   KEYWORDS
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Losses 1 to 9010)
Novitsky, V.A., Montano, M.A., McLane, M.F., Renjifo, B., Vannberg, F.,
Novitsky, V.A., Montano, M.A., Marlink, R. and Essex, M.
Foley, B.T., Ndung'u, T.P., Marlink, R. and Essex, M.
Direct Submission
Submitted (03.DEC 1998) Immunology and Infectious Diseases, Harvard Submitted (03.DEC 1998) Immunology and Infectious Diseases, Harvard School of Public Health, FXB-310, 651 Huntington Avenue, Roston, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zuranslation "MSARASRLKGHKEDHWERTRLEFGGRKGYMERHIVWASPFFFFFF
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PRDYVDRFYKTHRAEQASQEVKNWMTETLLVQNANPDCKTILKALGPAATLEEMMTAG
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1 (bases 1 to 9010)
Novitsky,V.A., Montano,M.A., McLane,M.F., Renjifo,B., Vannberg,F., Foley,B.T., Ndung'u,T.P., Rahman.M., Makhema,M.J., Marlink,R. and
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Molecular cloning and pnylogenetic analysis of human
immunodeficiency virus type 1 subtype C: a set of 23 full-length
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HIV-1 isolate C-96BW15CU2 country Botswana, complete genome.
AF110974
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Viruses, Ketroid viruses, Retroviridae, Lontivirus, Primate
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/gene-"gag"
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AAVKAAGWWAGTGGEFG IPYNGSGGOVESMIKET KR I IGGVEDGAEHLKTAVOMAVE
THNEKERGGTGGYSAGERT IUTTATDTGTKFF ØKGTTKFLGONFRVYPDSREDFIWKGPA
ALNPOLLET SEGOKO LMKOLOPALOTOT PELLESLENTVAT LYCVHPK LKVKLYTKEALD
                                    K TEFFUNKSGERT GQAFAAAGK TSGNYD EVGNI GOGMUHGA LSDFTT NAWVKV FPFRA
FSPEVI PMFTALSEGAT PQDL NI ML NI VOGHQAALQML KDT I NEEAAEWDR LHPVHAG
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KEGHTARNCKAPRKKGGWKCGN EGHOMKLICT ERQANFFREDLAFPQGKAREFPSEQNR
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AUEBHEKYHSNWMMAMASEFNLIPPLVAKETVASODKOQLKGEATHOQVDGSPGTWOLDC
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ESPHPKVSSFVHTPTGFARIVTTYWELGFEFEHHTGERGVSTEWELERYSTGVFPEL
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/qene:"vit"
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DTISLMDQSLACCYKLLELSVTLAGTINYSTINYSNTMALSYNNIFTGETKNCTENMTT
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3T SYMYTFSNSS LITT FOLTROLINMAQKVAFATYAPPT FONTTOSSSTTGLLLARDG
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AVTEGET GAAGGEMOAASTTI TAGAKGLLSGTVETEND FATEAKRPVVGFEKRAVGTG
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                                                                                                                                                                                                                                                                                                                                                                                                        STARSTALTOR "MYNELAARVOYPISVSALIVALIIA (VVWSTVY) ESEEMIRGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQYWGLELKKSATSLLIDSTATAVAEGTDRITEVIQRIYRAFGNIPRRVRQGFEAALD"
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oin(5436, .5511,7836, .8083)
qene "reg"
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Zproduct "Rev"
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/1990-"997"
5706.
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/qene "eng"
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/qene "net"
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/gene "ypu"
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SUIPPE

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OWTYOIYQEPFKNLKTGKYAKMRTAHTNOVKQLTFAVQKIAMESIVIWGKTPKFRLPI
OKETWETWWTDYWQATWIPEWEFVNTPPLVKLWYQLEKEPIIGAETFYVDGAANRETK
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PDKSESELVNQIIEQLIKKEKVYLSWVPAHKGIGGNEQIDKLVSKGIKKVLFLGGIDK
AQEEHEKYHSNWRAMASEFNLPPIVAKEIVASCDKCQLKGEAIHGQVDCSPGIWQLDC
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AAVKAACWWAGTQQESGIPYNPQSQGVVESMNKELKKTIGQVRDOAEHLKTAVQMAVF
THNFKPKGGTGGYSACRRIIDITATDIQSKELQKQTTKIQNFKVYYRDSRDPTWKGPA
KVLWKGEGAVVIQDNSDIKVVPRRKVKIIRDYGKQMAGADCVAGKQDED"
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RNM1.7QLGCTLNFPISPIETVPVKLKPGMDGPKVKQWPIJFEKIKAIJAICEEMEKEG
KITKIGPENPYNTPVFAIKKKDSTKWPKLVDFPFI.NKPTQDFWEVQLGIPHPAGI.KKK
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ALNPGLLETSEGCKOIVKQLQPALQTGTEELKSLFNTVATLYCVHEKTKVKDTKEALD
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GPGATLEEMMTACQGGGGGGGGGGKARVLAEAMSQATSANTLMORSNFKGPKRTTKCFNCG
KEGHTARNCRAPRKKGGWKGGKEGHQMKDCTERQANFFREDLAFPQGKAREFPSEQNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-DEC-1998) Immunology and Infectious Diseases, Harvard School of Public Health, FXB-310, 651 Huntington Avenue, Boston, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIEEEQNKSQEKTQQAEAAAGKISQNYPIVQNLQGQMVHQAISPRTLNAWVKVIEEKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novitsky,V A , Montáno,M.A., McTane,M.F., Renjifo,B., Vannberg,F., Foley,B.T., Ndung'u,T.P , Marlink,R. and Essex,M.
Direct Submission
                                                                                                                                             lentivirus group.
1 (bases 1 to 9010)
Novitsky,V.A., Montano,M.A., McLane,M.F., Renjifo,B., Vannberg,F.,
Foley,B.T., Ndung'u,T.P., Rahman,M., Makhema,M.T., Marlink,R. and
                                                                                                                                                                                                                                                                           Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Botswana J. Virol. 73 (5), 4427-4432 (1999)
                                                       Human immunodeficiency virus type 1.
Human immunodeficiency virus type 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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/protein_id="AAD17135.1"
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/country="Rotswana"
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AF110975 1 GT:4324731
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281. .1759
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                                  KEYWORDS
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    VERSION
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stilecasiakayekevhnvwaihacvetdenegeieldhvytchimwkndmvdomhe
biislwbqsikprvkliplcvytkcinystnysnimnatsynnyteeikncifnmtt
Elrdkkoovyaleykldivplnsnsseyrlincnisaliqacpkvsfdpipihycapa
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/translation="megapedggglefiberischerisimmorparnsasms"
YIYETYGDTRTGVKAIIRILQQLLFIBERISCLHSRIGIMMORPARNSASRS"
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                                                                                           VSILDIRÜGPKEPFRUTVDRFFKTLRAEQATÇDVKNWMTDTILVQNANPDCKTILRAL
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                                                                          PIAPGOMREPRGSDIAGTISTLQEQITWMTSNPPIPVCDIYKRWIILGLNKIVRMYSP
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/gene="rev"
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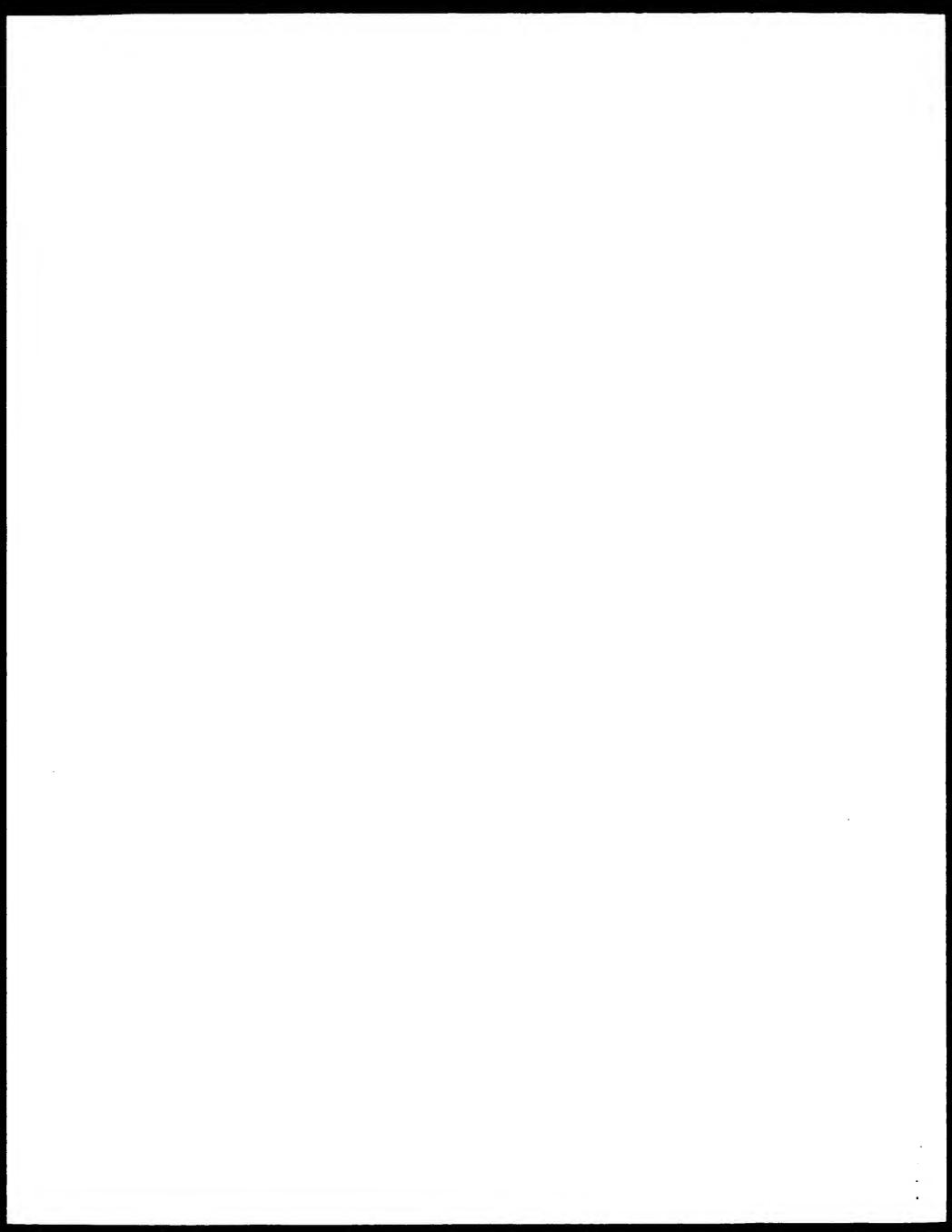
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QIQARVLAIERYLKDQOLLGIWGCSGKLICTITVPWNSSWSNKTQGEIWENNTWMOWD
KEISNYTGIIYRILEESONQQEONEKDILALDSRNNLWSWFNISNWLWYIKIPIMIVG
GLIGLRIIFAVLSIVNRVRQGYSPILSEQTLTPNPRGLDRIGRIEEEGGEODRDRSIKL
VQGFIALAMDDLRSLCLESYHRIRDLIIVTARVVELLGRSSPRGIQRGWEALKYLGSL
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SUMMARIES

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Submitted (12-JUL-2000) Chemical Pathology, Women's and Children's Hospital, 72 King William Foad, North Adelaide, SA 5006, Australia Location/Qualifiers
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YSPTSTLDTROGPKEPFRDYVDRPYKTLRAEGASGEVKNWMTETLLVQNANPD°KTTL
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isolate YU 2"
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87.8%; Pred. No. 5.7c-122;
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/organism="synthetic construct"
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/protein_id="AAG28738.1"
/db_xret="G1:11066867"
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AF202464 1847 bp DNA SYN 12-MAR-2000
Synthetic construct dag-professo fusion profein GP1 gene, complete
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           aggacectgeaggageagategectggutgumugmaneeceeeteecegtggage 774
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1 (bases 1 to 1847)
zur Megede,J., Chen,M.C., Doe,B., Schaefer,M., Greer,C.E.,
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KMYSPTSILDIRQGPKEPFRDYVDRFYKTLKAEQASQDVKNWMTETLLVQNANPDCKT
ILKALGPAATLEEMMTACQGVGGFGHKARVLAEAMSQVTNPATIMMQRGNFRNQFKTV
KCFHCGKEGHIAENGAFEKEGGWFGGFPFIHGMFPGTFFGANFLGKIWPSYKOPPGNF
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//t-auslation "MGAFASVLSGGELPKWEKIPLPPGGKKYKLKHTVWASPELFRF
//t-auslation "MGAFASVLSGGELFSEGSTNIVALLYCVHGRIDVKDTKEALE
AVNPGLLETSEGGRQ1LGQLQPSLQ1GSEELKSLYNIVALLYCVHGRIDVKDTKEALE
KIEEEQNKSKKKAQQAAAAAAGTGNSSQVSQNYPIVQNIGOGQWVHOAISPFLNAWVKV
Selby,M., Otten,G.R. and Barnett,S.W.
Increased expression and immunogenicity of sequence-modified human
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/protein_id="AAF42819.1"
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85.8%; Pred. No. 5.8e-117;
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/db_xref="taxon:32630"
                                                                               immunodeticiency virus type 1 gag gene
T. Virol 74 (6), 2628-2635 (2000)
                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (05-NOV-1999) Vaccines,
Street, Emeryville, CA 94608, USA
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zur Megede, J. and Barnett, S.W.
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Selby,M., Otton,G.R. and Barnett,S.W.
Increased expression and immunogenicity of sequence modified human
    Synthetic construct gag-protease fusion profein GP2 gene, complete
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/product="qaq-protease fusion protein_GPz"
/protein_id="AAF42820.1"
/db_xret="G1:7229427"
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/db_ared "taxon.32630"
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1. 1847
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RTBGAHTNIVKOIFFAVOKIAFESIVIWGKTPKFRIPIOKFTWWTFYWWTFYWOATWIPE
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AEVIPAETGGETAYFLLKLAGKWFVFTHTDNGSNFTSATVKAACWWAGTKQEFGTPY
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Fuller,M. and Anson,D.S.
Direct Submission
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S.hmitted (12-191-2000) Chemical Pathology, Women's and Children's
Hospital, 72 King William Road. North Adelaide, SA 5000, Australia
Hospital, 72 King William Road. North Adelaide, SA 5000, Australia
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/db_xref-"taxon:32630"
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Direct Submission
Submitted (12 JHL 2000) Chemical Pathology, Women's and Children's
Rospital, 72 King William Road, North Adelaide, SA 5006, Australia
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Anti-viral vectors Falcat: WO 3055341 A 2 21-SEP-2000; SDEN MARK (GR) : CXFORD RIOMEDICA LTD (GR) : MITROPHANOUS KYRIACOS 1308 ccaecaagggeegeeeeggeaactteetgeagageegeeegageeeaaeggeeerege 1367 1074 1129 aycaacttcaagggccccnggnqcalngtraaqtgnttnaartgcggcaaggagggccan 1188 1189 ategrecycaartgeegegeeereegeaaaaaaggrigeiggaagigeggeaaggagge 1248 gaceccategeereeggeragalgegregagreregregeageategeeggeace 714 757 AGGACCCTGGAGGAGAAGATAGATAGANISAÇAAAGAAÇAQAÇAAANAAAAAAGAGAGA 816 835 agcatectggaeateaagcagggeeecaaggageetteegegagetaegtgggggggffe 894 15-NCV-2000 955 ctyctygtycagaacyccaacccogactgcaaqaaccatectgegegetetctoggeeeege 1015 gecageetygayyaqatgatgaregeetgecaqqgeqtggqeqgerecagecacaqqee ttcaagaccetgegegeegageagageaceeaggaggtgaagaactggatgacgacace 937 TACAAGACCCIGAGGGCGGAACAGAGAGCAGGAGGIGAAGAAGAACIGGAIGACCGAGAGC ctgaaggacaccatcaacgaggaggergergagtgggarggegtgcaccccgtgcacqc PAT Sequence 2 from Patent W00055341. artificial sequence. 1 (bases 1 to 4307) Uden,M. and Mitrophanous,K. AX035453.1 GI:11191095 4337 bp synthetic construct synthetic construct 1417 AGGGAGAGGCAGGT 1430 1368 egagagetterget 1381 AX035453 AX035453 DEFINITION ORGANISM **NOTSEAUDY** KEYWORDS SOURCE REPERENCE AUTHORS JOURNAL AX035453 VERSION RESULT q ŝ qq Ś q δ Dp Ŏ δ g ŝ <u>q</u> ò 걾 ολ DP δŏ 67 5 á

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Location/Qualifiers
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Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
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Mitrophancus, F., Kingsman, A.T. and Kim, N.
Anti-viral vectors
Patent: Wr 9941397-A 2 19-ANG-1999;
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/note="pSYNGP4 codon optimised HIV 1 qaqpol with 20 bp of the leader sequence of HIV-1, etc"
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Patent: WO 0055341-A 14 21-SEP-2000;
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1 (bases 1 to 4427)
Uden,M. and Mitrophanous,K.
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1 (bases 1 to 4353)
Uden, M. and Mitrophanous, K.
Anti-viral vectors
Patent: Wo 005534i-A 13 21.SEP 2000;
UDEN MARK (GB) ; OXFORD BIOMEDICA LID (GB) ; MITROPHANOUS KYRIAGOS
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                                                                           Sequence 13 from Patent WOO055341.
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[ (bases 1 to 4642)
Uden,M. and Mitrophanous,K.
Anti-viral vectors
Patent: Wo 0055341-A 12 21-SEP-2000;
UDEN MARK (GB) ; OXFORD BIOMEDICA LTD (GB) ; MITROPHANOUS KYKIACOS
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/db_xret-"taxon:32630"
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Live. 0; Mismatches 297; indels 24;
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1 (bases 1 to 9007)
Novitsky,V.A., Montano,M.A., McLane,M.F., Renjifo,B., Vannberg,F.,
Foley,B.T., Ndung'u,T.P., Rahman,M., Makhema,M.J., Marlink,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Botswana J Virol 73 (5), 4427-4432 (1999)
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Viruses, Retroid viruses: Retroviridae, Lentivirus, Primate
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QKDTWETWWTDYWQATWIPEWEFVNTPPLVKLWYQLEKEPIAGAETFYVDGAANKETK
LGKAGYYTNKGPOKIVPLTETTNQKAELQAIQLALQDSGSEVNIVTDSQYALGIIQAQ
PDKSESELVTQIIEQLIKKERIYLSWVPAHKGIGGNEQVDKLVSSGIRKVLFLDGIDK
AQEFHEKYHCNWRAMASDFNLPPVVAKEIVASCDKCQLKGEAMHGOVDCSPGIWQLDC
THLEGKIILVAVHVASGYIEAEVIPAETGQETAYYILKLAGSWPVKVIHILNGSNFTS
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GPIAPGOMKEPKGSDIAGTTSTLQEQIAWMTSNPPIPVGDIYKKWIILGLNKIVRMYS
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LGEGASLEEMMTACQGVGGPSHKARVLAEAMSQANTSVMMQKSNFKGPPRIVKGFNGG
KEGHTARNCEAPFKKGTWKGREGHQMKDCTERQANFIGKIWPSHKGPPGNFLQSRPE
PTAPPAESFREEETTFGGNGESKUKETLTSLKSLFGNDPLSG"
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IHNFKRKGELGGYSAGEFIIRITATDIGTKELOKQIIKIONFPVYYPINSPPVWKGPA
KLLWKGEGAVYIQDNSDIKVVPRRKVKIIRDYGKQMAGDDCVAGRQDED"
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ALNPGLLETSEGCKQIIRQLHPALQTGSBELKSLFNTVATLYCVHFKIEVRDIKFALD
                                                                                                                                          Submitted (03-DEC-1998) Immunology and Infectious Liseases, Harvard School of Public Health, FXB-310, 651 Huntington Avenue, Boston, MA 02115, USA
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                        2 (bases 1 to 9007)
Nivitsky V.A. Montano, M.A.: McLane, M.E., Renjifo, B., Vannberg, E., Foley, B.T., Ndung u, I.P., Mailink, R. and Essex, M.
Direct Submission
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/protein_id="AAD17056.1"
/db_xref "GI.4324792"
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/protein_id="AAD17055.1"
/db_xref="G1:4324791"
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/db_xref~"taxon:11676"
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/db_xret="G1:4324796"
/1ranslation="MACPSCOSTFRALLGAVPILKILYQSNPYPEPEGTEQAPKNRRRR
WRARGRQIHSISERILSICLGRPTEPVPFOLPPIERLHINGSESSGASGTQQSGGTTE
GVGNP"
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WLVKRIRERAEDSGNESPGDTRELSIMVDMGHLPLLDDI"
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AGYATLKONNKTFNGLGPONNVSTVQCTHGTRPVVSTQLLLNGSLAEBELLTRSENLI
NNAKTTIVHLNESVRTECTGPNNNTRKSMRTGPGQFFYATGETVGDTRQAHCNISEKD
                                                                                                                                                                                                                                          Zprotein_id="AAD12058.1"
Zdb_vref="G1:4-6.4794"
Ztranslation="MERAPEDGPORGPYNEWALELLEELKOBAVREPRMMLHGLGO
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RATLEYASDARAYEREVENNWATHACVEFDENNOEVILENVIENENMENDMVEOMHE
DITSEMPOSELKPOVKLITELCVILINGTKVNGTSNYRGINNSSVPMEEEMKNGSFNI
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QTRVLATERYLKDQQLLGTWGCSGKLTCTTVVPWNNSWSNKSLNYTWENMTWMEWDRE
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HNOSNETFRPGGGDMKDNWKSELYKYKVVETKPLGTAPTEARKKVVEREKRAVGMGAV
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                YWGLELKKSATSTLUTTATAVAFGTDRITETAGRICRATGNVPTRIRQGFEAALQ"
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Submitted (03-DEC-1998) Immunology and Infectious Diseases, Harvard School of Public Health, FXB-310, 651 Huntington Avenue, Boston, MA 02115, USA
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Direct Submission
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Foley,B.T., Ndung'u.T.P., Rahman.M., Makhema.M.J., Marlink,R. and
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HIV-1 isolate C-96BW04.07 country Botswand, complete genome.
AF110963
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Novitsky,V.A., Montane,M.A , MeTane,M E
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PDKSESELVTQIIEQLIKKEPIYLSWVPAHKGTGGNEQVPKLVSGTRKVI-FILDGIDK
AQEEHEKYHCNWPAMASDFNI.PPVVAKFIVASCDKCQI.KGFAMHGQVDCSPGIWQLDC
THLEGKIII.VAVHVASGYIEAEVIPAETGQETAYYILKI.AGRWPVKVIHTDNGSNFTS
TAVKAACWWAGIQQEFGIPYNPQSQGVVESMNKELEKIIGQVREOAEHLKTAVQMAVF
IHNFKRKGFIGGYSAGEPIIDIIATDIQTKELGKQIIKIONFRYYRDSRDPVWKGPA
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PVSTLDIKCGPKEPPPPVDPFFKTLPAEQSTQEVKNWMIDTLLVQNANPDCKTILRA
LGPGASLEEMMTACGCVGGPSHKARVLGEAMSQANTNVMMQKSNFKGPRRIVKCFNCG
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AFSPEVIPMFFALSEGATPODLNTMLNTVGGHQAAMQMLKDTINEEAAEWDRVHPVHA
GPIAPCOMREPPGSPIAGTTSTIQEQIAWMISNPPIPVGDIYKRWIILGLNKIVRMYS
PVSILDIKQGPKEPFRDYVDRFFKTLRAFQSTQEVKNWMTDTLLVQNANFDCKTILRA
IGPAASILEEMMTACOGVGGPSHKAPVLGEAMSQANINVMMQKSNFKGPPRIVKCFNCG
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ADQLIHWHYEDCFADSAIRKAILGQIVSPROFYQAGHNKVGSLQYLALTALIKPKKRK
PPLPSVEKLVEDPWNFPQKTRGRRGNHTMNGH"
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PNMITOLGCTLNFPÎSPIETVPVKLKPGMDGPKVKÔWPLTEFKÎKALTAÎCEDMEKEG
KITKIGPENPYNTPVFAÎKKKDSTKWRKLLDFRELNKRTQDFWEVQÎ.GÎPHPAGLKKK
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KHQKEPPFIWMGYELHPDKWTVQPIOLPDKDSWTVNDIGKLVGKI.NWASQIYPGIRVR
HLCKLI.RGAKALTDIVPLTEEAFLELAENREILKEPVHGVYYDPSEDLIAEVQKQGHY
QWIYQIYQEPFKNLKIGKYAKMPTAHTNDVKQI.TEVVQKIAMESIVIWGKTPKFFRLPI
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ALNPGLLETSEGGRQIIRQLHPALQTGSEELKSLENTVATLYCVHEKIEVRDTKEALD
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ANSPTSRELQVPGNNPPSFTPVEGGGNFNPPOTTLWQRPIJVSTKVGGGTREALLDTGA
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/translation="MGARASILRGGKLDAWERIRLRPGGKKCYMMKHLVWASPF1FKF
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                                                             /organism="Human immunodeficiency virus type 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="gag-pol polyprotein"
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join(280. .1563,1563. .4562)
/codon_start=1
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/protein_id="AAD17037.1"
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                                                                                                                         /isolate="c-96RW04.07"
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                                                                                                                                                                                      /country="Rotswana"
/note="subtype: C"
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/qene="vpr"
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/qene="vif"
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/qene="vif"
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/gene="gag"
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ISYGKKKFPGGFSTPPSSEDH_UNPVSKQPLSQTRGDFTGSEESKKKVESKTEADPFD"
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Ztranslation="MAGRSGDSDEALLQAVKLIKILYQSNPYPKPEB-IRQAKNRERE
WRARQEQIHSISEKILSFCLGRPTEPVPFQLPPIERLHINGSESSGASGTQRSQGTTE
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zab.vrof="at;4324779"
ztransiarion="mistaatnyktovgaevvaltiativwityyteyrktvrokkid
wlvkmireraedsgresdodieelstrwumghfrliddi"
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I GLEFTFAVLS I VNRVROGYSPLISFOTL. I PNPRKSDRLGR I EEEGGEODRGKS I KLVS.
GFLALAWDDLKSI CHESVHRFRDFILLIAARAAFT I GRSGI ROTQROWELLERFUST VQ.
YWGLELER SATSTI DITATAVAFT I DETTATAVAET I GRSGI ROTGROP IP I PGGEEAALQ."
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DNAKTTIVIILNESVRTECTGPNNNTRKSMRTGPOQTFYATGFTVGDTPQAHCNTSEKD
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DESYWSNNITRETINFPPEROTINWYSOOFRIYAPETAONITOVSNITOLITUWOO
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OTRVLATERYLKEXGELLGT WGYSGKLT CTTNVPWNNSWSNKSLNYTWENMTWMEWDRE
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/translation="madkwsksstvawpavefemepaafdvotaspidlikydale
                                                                                                                       Zi Justation : "MERAPEDGGLOREPYNEWALELLEELKGEAVRHEPRMMLHGLGQ
YTYETYGDIWTGVEALLIRTLGGLLFTHFRIGGGHSRIGILRORRVRNGTNRS"
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DTTSLWOOSLKPCVKLTPLCVTLNCTKVNGTNGTSNTKGTNNSSVPMEEEMKNCSFNT
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                                                                                                                                                                                                                       Join(5295, .5510,7833, .7923)
Zgene-lat.
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/qene-"rev"
/codon_start+1
/product*"Vpr"
/protein_id="AAD17040.1"
/db_xret="G1:4324776"
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/product="Env"
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5534, ...5785
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/qene="env"
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/qene."net"
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|| HELLITE FIELT || HELLITE EL TE || HELLITE EL
760 GCTTICAGCCAGAGGTAAFACCAFGTTAAAGCATATAAAGAAAGAAGGAAGAAAA 819
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Submitted (03-DEC-1998) Immunology and Infectious Diseases, Harvard
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Direct Submission
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1 (bases 1 to 9036)
Novitsky,V.A., Montano,M A , McLane,M F , Renjifo,R , Vannberg.F.,
Foley,B.T., Ndung'u,T P , Rahman,M., Makhema,M.J., Marlink,R. and
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                                                                                                                                      1021 etggaagagatgatgaeeqeetgeeagggegtgggeggeerreageracaaggeegegtg 1080
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1300 TTAGAAGAAATGATGAGAGGATGTGAGGGAGGAGGACCTAGCCAGAAAGCAAGAGTT 1359
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Viruses: Retroid viruses: Retroviridae: Lentivilus, Primate
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CPIAPSQMPFPPGSDIAGTTSTLQFQTAWMTSNPPIPVGDIVKHWITGLNKIVRMYS
PVSILDIKQGPKEPFPDYVPPFFKTLRAEQSTQEVKNWMTDTLLLVQNANPDCKTILRA
LCPGASLEEMMTACQGVGGPSHKARVLAEAMSQTNTNVMMQRSNFKGPRRIVKCFNCG
KEGHIARNCRAPRKKGCWKCGKEGHQMKDCTERQANFLGKIWPSHKGRPGNFLQSRPE
PTAPPAESFRFEETTPVQKQEPKDRETLTSLKSLFGSDPLSQ"
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Esrhppvssevhiplgdarlytktywgiqtgepiwhlahgvsiewhirkysiovdpgp
Adqliimhyfucfadsairkailgqivsprceyqaghnkvgslqylaltalikpkkrk
Pplpsvrklyedrwnepqktrgppgnhtmngh"
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DDTVLEDINLPGKWYPK11GGIGGFIKVPQYEQILLELGGKKA1GIVLVGPTPINIIG
PNMITQLGCTUNPPISPIETVPVKLKPGMDGPKVKQWPLTEEKIKALTAICEEMEKEG
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AAVKAANWAATTOOFFGTPHNPQSQGVVESMNKELKKTIGQVREQAEHLKTAVOMAVF
THNPKRKGGTGGYSAGERTIDITATDIQFKELOKOLLKTQNFKVYYRDSRDPVWKGPA
KLLWKGEGAVVIQENSPTKVVPPKKVKTTPPGKQMAGFGFVAGRODED"
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GPIAPGOMREPRGSDIAGTTSTLOEQIAWMTSNPPIPVGDIYKRWIIIALNKIVRMYS
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LGPGASTERMMTAGGVGGPSHKARVLAEAMSQTNTNVMMQRSNFRGPRRTVRCFNCG
REGHLARNCEAPPRREGSWRGGPFRBGMKPGTEPGANFFPENTAFPGGPAPEFPSFGTP
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SSMTKILEPFRTKNPDIVIYQYMDDLYVGSDLEIGQHRAKIEELREHLLKWGLTTPDK
KHQKEPPPLWMGYEIHPPNWTVQPTQLPDRPSWTVNDIQKLIGKINWASQIYPGIRYK
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KIEEEGNYGGGYTQQAFAAOKGKVSQNYPIVQNLQGQMVHQAISPRTLNAWVKVIEFK
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                                                                                                                                                                                                                                   /product="gag-pol polyprotein"
/protein_id="AAD17047.1"
/db_xref="G1:4324783"
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ENLTDNAKTTTVHLNKSVETVCTRPNNNTEKSVRTGPGGTFYATGALTGNTRQAHCNI
SGDKWNETLHWVSTKLAEHFPNKTTRFNSSSGGGLFTTTHSFNGPGFFFYGNTSGTFN
ESYWENETYGSNGTRATTTLDCRTKOTTNWWGGVGPAMYALPTAGNTTGKSNTTGLLL
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LTVWGTRQLQTRVTATPPYLKPGGLLGTWGPSGRTTFTTVVPWNNSWSNKSTPYTWSN
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Score 797.4; DB 58; Length 9036;

51.98; Score 797.4; DB 71.28; Pred. No. 1e-81;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is delived by analysis of the total score distribution

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ive 0: Mismatches 756; Indels 22;
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Unpublished (2000)
Contact: Muller Miklos
Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
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HVSMEf0019H19f Hordowm vilgare seedling root EST library HVrDNA0007
(etiolated and unstressed) Hordowm vulgare cDNA clone
HVSMEf0019H19f, mRNA sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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Wing,P . Close,T J , Kleinhofs.A., Wise,R., Bequm.D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernedle,S., Palmer,M., Rambe,
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
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                                                               913 cosoproroassasspectrosectiostastracecesstracamistracadalered 972
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853 ACGIGCIGGICAICCIGACGGACAIGICGICGIACGCGAIGCGTGGGGGGGGAGATTCICGG 912
                                  830 igagealectygaealecyceagyyceceaaygayeeetteeyeyactaeytygaeeget 889
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Clemson University
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HG314500 509 bp mRNA EST 16-APR-2001
WHE2495_E11_I2122 Triffoum mononcoum marly reproductive apex CDNA
library Trifficum mononcoum cDNA clone WHE2495_E11_I21, mPNA
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/clone_lib="Hordows vulgare seedling root EST library
HVcDNA0007 (etiolated and unstressed)"
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100 Jordan Hall, Clemson, SC 29634, USA
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/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism."Hordeum vulgare"
                                                                                                                                                                                        Email: rwing@clemson.edu
Sejprimer AATTAACGGG
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/db_xref="taxon-4513"
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282 c l
                                                           Tel: 864 656 7288
Fax: 864 656 4293
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/dev_stage "Seven week old plants"
//dev_stage "Seven week old plants"
//dab_host="E, coli XLOLR"
//dab_host="E, coli XLOLR"
//dab_host="E, coli XLOLR"
//dab_host="EcoRI; Site_2: Xhol; The tissue, total kNA, and
Site_1: EcoRI; Site_2: Xhol; The tissue, total kNA, and
poly(A) RNA were prepared from apex at double-ridge stage
to terminal-spikelet stage during transition from
vegetative state to tlower state, a cDNA library was made,
and the cDNA clones were in vivo excised at the
University of California, Davis (V. Echenique, B. Stamova
, J. Dubrovsky). Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
                                                                                                                                                                                                  Eukaryota, Viridiplantaes Streptophytä, Embryophytä, Tracheophyta;
Spermatophyta, Magnellophyta, Lilliopsida, Poales, Poaceae, Pooldeae
, Triticeae, Friticum.
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US Department of Agriculture, Agriculture Research Service, Pacific
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The structure and function of the expressed portion of the Wheat genomes - Early reproductive apex cDNA library from Triticum
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/db_xrof "taxon:4568"
/clone="WHE2495_E11_121"
/clone_lib-"Triticum monococcum early reproductive apex
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800 Bachanan Street, Albany, CA 94710, USA
961: $105595773
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US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773
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//note-"Vector: Lambda Uni ZAP XR, excised phagemid;
Site_l: EcoRI; Site_2: Xhol; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and
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/note="syn. Phreatamoeba balamuthi"
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cDNA clones (expressed sequence tags) from the free-living amitochondriate amoeboflagellate, Mastigamoeba balamuthi
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/strain="ATCC 30984"
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1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 1327 Std Error: 0.00
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Contact: Muller Miklos
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Best Local Similarity 44.1%; Pred. No. 0.0023;
Matches 395, Conservative 0, Mismatches 492; Indels
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                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trachcophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Iriticeae, Triticum.

1. (bases 1 to 648)
Anderson, O.D., Chao, S., Han, P.S., Hsia, C.C., Johnson, R.R, Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L., Iong, J.C., Verhey, S.D. and Walker-Simmons, M.K.
                                                                                                                                                                                                                                                                                                                              Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
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/clone_lib:"Wheat ABA-treated embryo cDNA library"
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49.1%; Pred. No. 0.0028;
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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The HDGP brosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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Submitted (62 JGN 1999) Genesemper - Centre National de Sequencage :
BF 191 91006 EVRY cedex - FKANCE (E mail : seqret@genoscope.chs.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genome survey sequence 17 end of BAC # BACK14B09 of RPC1 98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Tel: (613) 759-1662
Fax: (613) 759-1701
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit
1124 agaaggaactteaagggeeeeeggegaegteaagtgetteaactgeggeaaggagg 1183
                                                                                                                                               1184 gecacategecaaqaaetyeeqeqeeceeeqeaaqaaaggetgetggaagtgeggeaagg 1243
                                                                                                                                                                                                                                                                                              1244 agggccaccaqatgaaggactgcaccgagcgccaggccaacttorfgggraagatotggc 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                           1304 ccagocacaagggcogcocoggcaactroctgcagacogcagogagocagoogcogcocca 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1364 cogigocoacogococococogothagagetinogeticagagagacoacococogotococa 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1424 agcaqqageccaaggaccqcgagccetaccgcgaycccctyaccyccttgcgcaycctgt 1483
                                                                                                                                                                                                                                                                                                                                              644 productivities of the contractive of the contractive of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the contractivities of the cont
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                                                                                                                                                                                                                    513 CUCYCGBUCCCCCCCCCGCCMGCMVGCCMCCCMGVMAUCMGUGVGMMGMGMGMGRCVSSAGSG 454
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16.2%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydioidea, Diosophilidae, Drosophila.
1 (bases 1 to 1101)
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Matches 71; Conservative 197; Mismatches 171; Indels
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/note="end : SP6"
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AL108460.1 GI.5628764
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/tissue_type="Leaf, crown"
/note="Vector: Bluescript SK-/Xhol-EcoRI; Site_1: Eco RI; Site_2: Xho I; Lower temperature 50 C / hour from 22 to 120C, bring to 50 in 1 hour from 120C. Leave at 50C 3 days photoperiod 16 hours. Light intensity was 125 uE-1. Library prepared by in vivo mass excision from amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryóta, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta, Magnollophyta, Liliopsida, Poales; Poaceae; PACC clade, Panicoldeae, Andrópogomede, Zea.

(bases 1 to 813)
Singh,J.A., Wakui,K., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.

Expressed Sequence Tags from Cold-Stressed Maize Seedlings
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/clone_lib="Zm04_AAFC_ECORC_cold_stressed_maize_seedlings"
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960 Carling Arenge, R1dg 20. Ottawa. Ontario, K1A 006, Canada
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                                                                                                                                             71 geggeaagaageactacatgrigaageacetggtgtgtgggeeageegegagetggaaget 130
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                                                                     ESP JASSONORSISSISSISSISTERRINGAPVOTAGGGGASTACMAADOGGGATARACCSSS 717
11 gegecageatectgryrggryagaagntgganaagtgggagaagateegeetgegeeeg 70
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Bastern Cereal and Oilseed Research Centre
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/db_xref="taxon:4577"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 585)
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AL555284 LTL_FL013_FBIRT Homo sapiens clone CSODF0C3F107 3
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                                                                                                                                                                                                              94 ACCAGGGGACGAGGGGGGGGGGGGGGGAGCKGGAGGCGAACGGGAACGGGGAAGGGGG
                                                                                                                                                                                                                                                                                                         154 AAGACGESGCACTCCGGAGGTCGGCACAAGAGCCTTCCCAAGAGCCACGACCTCYACCAG 213
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4.4%; Score 56.2; EB 152; Longth 813;
Best Local Similarity 43.2%; Pred. No. 0.015;
Matches 409; Conservative II; Mismatches 389; Indels 6;
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Full-length CDNA libraries and normalization
Unpublished (2001)
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AL565284
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pcMVSPORT 6 vector. Library was constructed by Lite lechnologies, Centact; Fend Liang Lite Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Margland 20850, USA Fax. (1) 401-610-8371 Email:
                                                                                                                                                                                                                                                                                                                                               /note-"Organ: Fetal brain; Vector: pCMVSPOKT 6; 1st strand
cDNA was primed with a Not1-oliqo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not 1
and cloned into the Not 1 and Eco KV sites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determination of this BAC end sequence was carried out as part of a collaboration with the Berkeley Prosophila Genome Project (BBGP).
                                                                                                                                                                                                                                                    /dev_stage-"pooled rissue from post conception letuses (20 week, 24 week and 26 week)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        centre National de Sequencade :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACKIYD16 of REC1-98 library from Drosophila melanogaster (fruit 11y), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1262 actgracogagogocaggeraacttootgggeraagatetggeroageriscadggeger 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1382 cogeogagagetteogottegaggagaeceaeceeeceeecaageagagcocaagaee 1441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 CSSCCCAGGCCAGSCACCACTCCACCCACCACCACACACACACACACSACCYGS 267
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Eteryqota, Neoptera, Endopteryqota, Diptera, Brachyera,
Museomorpha, Ephydroidea, Drosophilidae, Drosophila,
BP 191 91006 EVRY codex - France
Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 4.4%; Score 66; DB 106; Length 585; Local Similarity 44.7%; Pred. No. 0.016;
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/clone_lib-"LTI_FL013_FBrn1"
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                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                         /db_xref-"taxon:9606"
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                                                                Gocation/Qualifiers
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Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Pesourre Center can be
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Eukaryota; Metazoa; Chordata; Craniata; Vertebiata, Euteleustumi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 901)
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BP 191 91006 FVRY cedex - France
Email: segref@genoscope.cns.fr, Web · www genoscope cns.fr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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14.4%; Pred. No. 0.016;
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Matches 52; Conservative 172; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
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Unpublished (2001)
Contact: Genoscope
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was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
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                                                                                                   /clone_lib="LTT_NFL006_PL2"
/tissue_type="placenta"
/note="vector: pCMVSFOKI 6; Site_l: Not1, 1st strand cDNA
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Bost Local Similarity 45.1%; Pred. No. 0.019;
Matches 274; Conservative 2; Mismatches 331; Indels 1:
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http://fulllength.invitrogen.com"
311 c 362 g 28 t
                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                 /clone="CSODIO41YA05"
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/clone_lib-"Mastiqamoeba balamuthi lambda ZAP II Library"
/note-"syn: Phreatamoeba balamuthi"
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Mastiqumoeba balamuthi eDNA similar to pyrophosphate--fructose
6-phosphate 1-phosphotransferase, mRNA sequence.
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                                                                                                                                                                                                                                               connection (expressed sequence tags) from the free living
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Unpublished (2000)
Contact: Muller Miklos
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43.4%; Pred. No. 0.021;
ive 0; Mismatches 521; Indels 9;
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                                                                                                                                                                                                                                                                                                                                                    The Rocketeller University
1240 York Avenue, New York, NY 10621, USA
                                                                                                                                                                                                                                                                                                                                                                                             Email: mmullerarockvax.rockefeller.edu
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1 (bases 1 to 1427)
                                                                                                                          Mastigamoeba balamuthi.
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                                                                                                                                            Mastigamoeba balamuthi
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Matches 407; Conservative
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spermatophyta; Magnoliophyta; Liliopsida, Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
1    (bases 1 to 777)
Wing,R., Close,T.J., Kleinhots,A., Wise,R., Bequm,D., Frisch,D., Yu,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Kambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
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BVSMEH0082E06f Hordeum vulgare 5-45 DAP spike EST library
BVcDNA0009 (5 to 45 DAP) Hordeum vulgare CDNA clone HVSMEH0082E061,
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Contact: Wing RA
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hvcnNAGOUS (5 to 45 DAP)"
/Lissue_type="5-45 DAP Spike"
/lab_host="Solk"
/note="Vector: lambda2AP; Site_l: Brokl; Site_2: Xhol"
1 248 c 272 q 101 t 2 others
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
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/db_xref ="taxon:4513"
/clone="HVSMEh0082E061"
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Seq primer: AATTAACCTCACTAAAGGG
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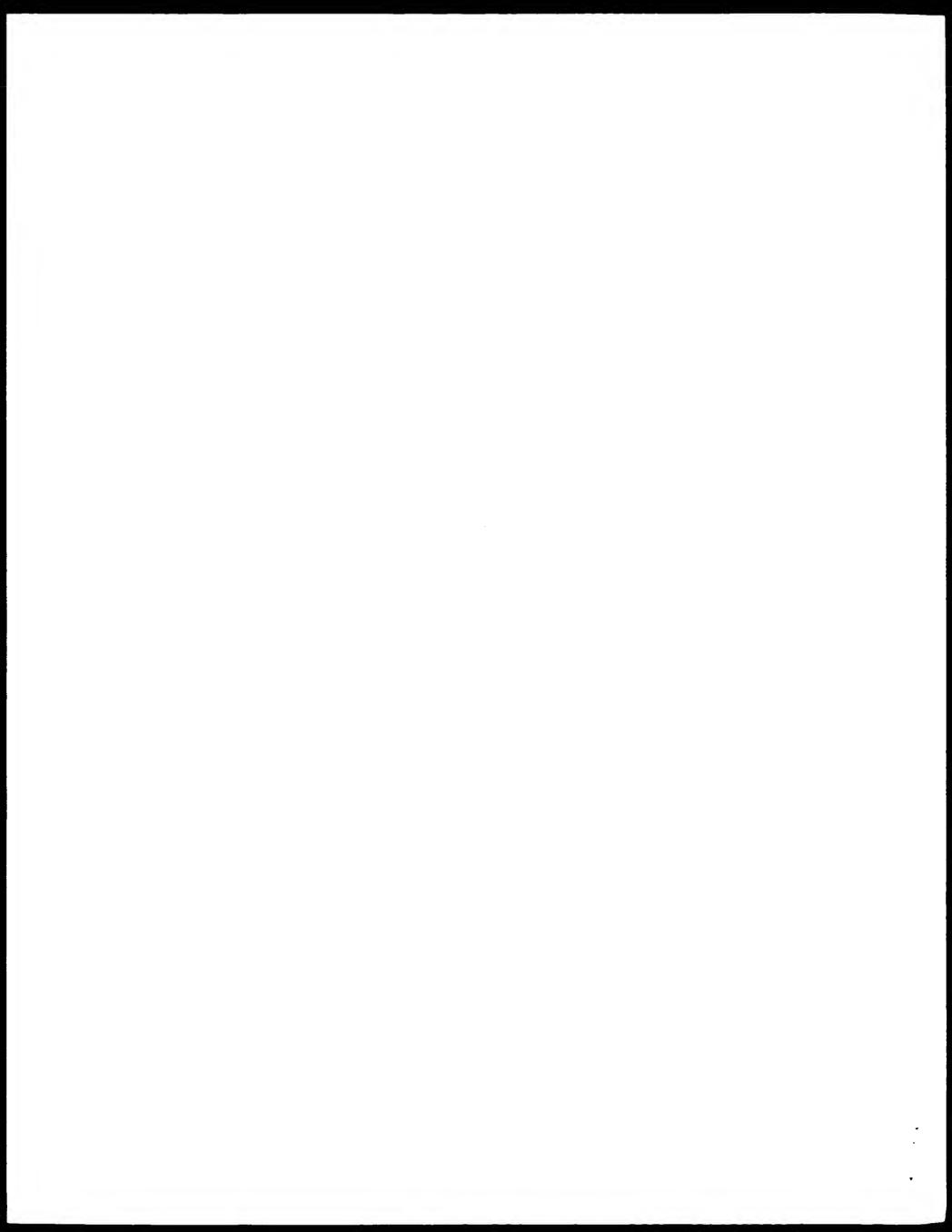
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta: Tracheophyta:
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pocideue
; Triticeae; Triticum.
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US Department of Agriculture, Agriculture Research Service, Pacific
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The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
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Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
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                                              Gaps
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
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/clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
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C
4 3%; Score 64.8; DB 164; Length 777; §0.6%; Pred No. 0.027;
                                             0; Mismatches 152; Indels
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800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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/db_xref="taxon:4565"
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Location/Qualifiers
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          Query Match
Best Local Similarity 50.69
Matches 156, Conservative
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Search completed. August 8, 2001, 20:59:47

Job time: 21891 sec

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greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the fJ close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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GenGore version 4.5
Copyright (c) 1993 / 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		 $ar{\Gamma}_{1}$, which desires the properties of			0086324666999999999999999999999999999999999
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ALIGNMENTS

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Eukaryota, Viridiplantae: Streptophyta: Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida: Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1. (bases 1 to 759)
Wing, K., Close, T.J., Kleinhofs, A., Wise, K., Begum, D., Frisch, D., Yu, Y., Anderson, H., Daie, J., Henry, D., Kornodie, S., Palmer, M., Fambo.
                                                  HF259495 759 bp GANA EST 23 EEB 2061
HVSMEt0019H191 Hordeum zulgare seedling root EST library HVcDNA0007
                                                                                                  (etiolated and unstressed) Hordeum vulgare CDNA clone
                                                                                                                          HVSME10019H191, mKNA sequence.
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                                                759 LE
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LOCUS
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                                                                                                                                                                           VERSION
RESIDE
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J., Saski, C., Schwaffzbock, J., Simmons, L., Choi, D.W., Main, D. and Wood, T.
                                                     Development of a genetically and physically anchored EST resource
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282 c 184 q 133 t 2 others
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HVCDNAC007 (ctiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host:"TJCl21"
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Unpublished (2000)
On Nov 16, 2000 this sequence version replaced qi:11188608.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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                                                                                                                                                                                                                                                                                                                                                                                                        /organism."Hordeam vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /elone-"HVSME10019H191"
                                                                                                                                                                                                                                                                                         Email, rwingstlenson.edu
Seq primer: AATTAACCCTCACTAAAGG
                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 757
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poly(A) RNA were prepared, a CDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the T close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                Eukaryota; Viridipluntae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US Department of Agriculture, Agriculture Research Service, Pacific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and
                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 562)
Anderson, O.D. , Chao, S., Choi, D. W., Close, T.J., Fenton, R. D., Han, P.S., Hsia, C., Kang, Y., Lazo, G.R., Miller, R., Rausch, G.J., Seaton, C. L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
                                             RF484304 562 bp mPNA EST 06-DEC-2000
WHED311_F11_K131S Wheat pfo authesis spike con library Triticum
aestivum cDNA clone WHED321_F12_K23, mPNA sequence
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/clone_lib="Wheat pre-authesis spike cDNA library"
/tissuc_type="Spike before anthesis"
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800 Buchanan Street, Albany, CA 94710, USA
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/db_xref="taxon:4565"
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/lab_host="E. coli SOLR"
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Eukaryota; Viridiplantae: Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida, Poales; Poaceae; Pooldeae
; Triticeae; Hordeum.
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(20 DAP) HOTGGUM VULGATE CENA CLORE HVSMEIOOZINZAÉ, MRNA SEGUEDCE.
BG369139
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422 igosecaggggathayahnnngdacettgaacgeetgggiqaaggitgaicgaygagaagg 481
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Pred No 0 0004;
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Seg primer: AATTAACCCTCACTAAAGGG
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/db xref="taxon:4513"
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	Contact: Olib Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Fel: 5105595773	DP 3	ω.

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Jaote "Vector: pGAD10; Site_1: Ecokl; Site_2: XhO1; Embryos were cut Irom mature, dormant seeds and imbibed in 25 microm ARA (abseisic acid) in 5 mM Mes butter, pH 5.7, for 12 hr at 22 °C. The tissue, total RNA, and poly(A) ENA were prepared by Steven Verhey in M.K. Walker-Simmons's lab (USDA-ARS, Washington State Univ., Puilman, Washington 99184-6420 A conA library was made by Clontech using a combination of random and oligo dT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Triticum aestivum"
/cultivar "Brevor (soft, white, winter, common wheat)"
/db_xret-"Taxon:4565"
/clone="WHE0616_A12_B24"
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                                                                          Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer; Clontech Matchmaker 3' AD primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib-"wheat ABA-treated embryo conA library"
/tissue_type "Seed embryo"
/dev_stage="Mature dormant seeds"
/lab_bost "E. coli DH12S"
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Email: oandersnapw.usda.gov
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558 SCSSA 554
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                                                                                                                                                                                                                                                                                                                                                                                                               when www genoscope cas. fr. betermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Fioject (BDGF). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopteryyota; Diptera; Brachycera,
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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Best Local Similarity 15.9%; Pred. No. 0.0026;
Matches 58; Conservative 178, Mismatches 126; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
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/dev_stage:"salt stress"
/lab_host="E. coli XL Gold"
/note="Organ: root; Vector: pBluescriptII SK(+) XR:
Seedling stressed root cDNA library from Wang/Bohnert lab"
164 c 227 q 115 t 2 others
                     stressed root cENA library from Wang/Bohnert lab
                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Emhryophyta, Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae, Andropogoneae, Zea.
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/tissue_type="seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.7%; Score 69.2; DB 102; Length 595; 48.5%; Pred. No. 0.0032;
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0; Mismatches 290, Indels
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/cultivar="B73"
                                             Zea mays cDNA, mRNA sequence.
A1857214
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Plate: 603008 row: P column
Location/Qualifiers
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Matches 284; Conservative
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Unpublished (1999)
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Fax: 650 725 8221
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TCATCGCTA agatgctgaa llll	EST 27 FEB 25 set dlings noe. phytu, Embryophyta, Track- iopsida, Poales, Poaceae;	Couroux, P., De Moors, A., Harris, L.J., Ha cobert, L.S., Sprott, D. and Tinker, N.A. ags trom Cold-Stressed Maize Seedlings bilseed Research Centre Frood Canada Bldg. 20, Ottawa, Ontario, KlA 0C6, Canada	ngnjarem.aqr.ca. Location/Qualifiers 1813 Aorganism="Zea mays" Acultivar="CG328" Abb_xret*"taxon:4577" Aclone="Zm04_03q03" Alisae_type="Leat, crown" Anste_1ype="Leat, crown" Anste_1ype="Leat, crown" Anste_1ype="Leat, crown" Anste_1ype="Leat, crown" Anste_1ype="Leat, crown" Anste_1ype="Leat, crown" Anste_1ype="Leat, crown" Anste_2: Xbo 1; Lower temperature 5c C / hour from 22 to Site_2: Xbo 1; Lower temperature 5c C / hour from 22 to Location to 5o in 1 hour from 120C. Leave at 5cC 2 days approperiod 16 hours. Light intensity was 125 uE-1. Uibrary prepared by in vivo mass excision from amplified	104 t - 24 others	.57
489 quenticuquerorgungitatoreralgits accidencidade quoque que cocca 1 1 1 1 1 1 1 1 1	EST 27.FEB 2501 2m64_3461_R Zm04_AAFC_ECECEC_vold_stressed_maize_seedlings Zea ma cDNA_clone Zm04_03q03, mRNA_sequence. BG321263 BG321263 GFF1350941 EST. Zea mays. Zea mays. Zea mays. Spermatophyta: Andropogoneae; Zea. Embryophyta, Ziacheophyta Clade, Famicoideae; Andropogoneae; Zea.	l (bases 1 to 813) Singh,J A , Wakul, K , Couroux, P., De Moors, A., Harris, L.J., J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A., J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A., Grandstein Seed Sequence Tags from Cold-Stressed Maize Seedlings Unpublished (2001) Contact: Singh,J A Eastern Cereal and Oilseed Research Centre Agriculture and Agri-tood Canada 960 Carling Avenue, Bldg. 20, Ottawa, Ontario, KIA 0C6, Carling (613) 759-1662 Fex: (613) 759-1662 Fex: (613) 759-1701 Feward Contactions and Contaction	: Singnjarem.aqr.ca. Location/Qualifiers 1. 813 /orqanism="Zea mays" /cultivar="C0328" /db_xref+"taxon:4577" /clone="Zm04_03q03" /clone_lib+"Zm04_03q03" /tissue_type="Leaf, crow/note-"Vector: Ribestrip Site_2: Xbo 1; Lower tem 120C; bring to 50 in 1 h, photoperiod 16 hours. Library prepared by in v	library." 174 a - 296 c - 215 g - 10	y Match Local Similarity 42.5%; Score 59.2, DB 152, Length 813, Local Similarity 42.5%; Pred. No. 0.0033; hes 34.3; Conservative 14; Mismatches 44.3; Indels 6; Ga 255 gtactgcqtqqqqqqqqtcqqqqqqqqqqqqqqqqqqqqq
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Spermatophyta, Magnellophyta, Lilliopsida, Poales, Poaceae, Pooldeae
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(bases 1 to 509)

Anderson, O.D., Chao, S., Dubcovsky, J., Echemique, V., Han, P.S., Hsia, C.C., Kanq, Y., Lazo, G.R., Miller, R., Ransch, C.J., Seaton, C.L., Stamova, B. and Tong, J.C.

The structure and function of the expressed portion of the wheat genomes - Early reproductive apex cDNA library from Triticum
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Clemson University
100 Jordan Hall, Clemson, SC 29634. USA
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/cultivar-"Morex"
/db_xref="taxon:4513"
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Matches 278; Conservative
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Contact: Wing RA
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/clone="WHE2495_E11_121"
/clone_lib="Triticum monococcum early reproductive apex
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                                                                                                       Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 seq primer: Stratagene SK primer.
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      West Area, Western Regional Research Center
                       800 Buchanan Street, Álbany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
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                                                                                           Email: oandersn@pw.usda.gov
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
HVSMEh0089C0lt Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0υύν (5 to 45 DAF) Hordeum vulgare cDNA clone HVSMEhnnxur0lf,
mRNA sequence.
BE195387
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/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note-"Vector: lambda2AF; Site_1: EcoR1; Site 2: Xho1"
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29-SEP-2000

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                                                                                                                                                                                                                                                                                                /clone_lib="Hordeum vulgare 5.45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP spike"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: lambdaZAP, Site_1. EcoR1, Site_2. Ahol"
226 c 247 g 115 t 3 others
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11
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unpublished (2000)
On Jun 26, 2000 this sequence version replaced q1:8705365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.5%; Score bo.2; DB 164; Length 770; Best Local Similarity 47.3%; Pred. No. 0.012; Matches 274, Conservative 6; Mishatches 254, indels 12.
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Tel: 864 656 7288
Fax: 864 656 4293
                                 Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                   /organism="Hordeum vulgare"
                                                                                                                                                           Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 659.
Location/Qualifiers
                                                                                                                                                                                                                                                                   /db_xref="taxon:4513"
/clone="HVSMEh0080B021"
                                                                                                                                                                                                                                                    /cultivar="Morex"
                                                                                                                                              Email: rwing@clemson.edu
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RESULT 12 AV391237

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Yana 1532-3, Kisaradu, Chiba 292-0812, Japan
Email ynakamuakagusa orijp. UPL-http://www.kazusa orijp/en/plant/.
Location/Qualifiers
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Chlamydomonadaccae; Chlamydomonas.

I (bases I to 599)

Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S.

A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags

DNA Res. 6 (6). 369-373 (1999)
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/dev_stage="photoautotrophic growth"
/nofe="Vertor: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS BES17190 627 bp mRNA EST 08-AMG-2000
DEFINITION WHEU615_FUZ_LU32A Wheat ABA-treated embryo cDNA library Triticum
                                                                                                                                                     Eukaryota, Viridipiantae, Chlorophyta, Chlorophyceae; Volvocales;
         AV 01237 Chlamydomonas reinhardtii 09 Chlamydomonas reinhardtii
CDNA clone CMUb9CU7_r, mKNA sequence.
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Kazusa DNA Research Institute
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/clone="CM069c07_r"
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                                                                                                                   Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
                                                            AV391237
AV391237.1 GI:6545453
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Best Local Similarity 47.8%;
Matches 192; Conservative (
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// Alb_host-"E. coli DHi2S"
// Alb_host-"E. coli DHi2S"
// Alb_host-"E. pGADI9; Site_1: ECOKI; Site_2: XhoJ;
// FUNCTOR: pGADI9; Site_1: ECOKI; Site_2: XhoJ;
// EMBLYOS Were cut from mature, dormant seeds and imbibed in 25 microM ABA (abscisic acid) in 5 mM Mes buffer, pH 5.7,
// FOR 12 hr at 22 C. The tissue, total RNA, and poly(A)
// KNA were prepared by Stetch Verbey in M.K.
// Walker-Simmons's lab (USDA ARS, Washington State Univ.,
// PUllman, Washington 99164-6420 A CDNA library was made
// by Clontech using a combination of random and oligo dr
                                                                                                                                                                                                Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Pooldeae
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West Area, Western Regional Research Center
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                                                                                                                                                                                                                                                                                                                             Anderson, O.D., Chao, S., Han, P.S., Hsia, C.C., Johnson, R.R., Kang, Y., Lazo, G.K., Miller, R., Rausch, C.J., Seaton, C.L., Tong, J.C., Verhey, S.D. and Walker-Simmons, M.K.
The structure and function of the expressed portion of the wheat
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/db_xref "taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="WHE0615_F02_L03"
/clone_lib="Wheat ABA-treated embryo_cDNA_library"
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destivum cDNA clone WHE0615_F02_L03, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            800 Buchanan Street, Albany, CA 94710, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Oandersnapw.usda.gov
                                                                                                                                                                                                                                                                  : Triticeae; Triticum.
1 (bases 1 to 627)
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                                                       RE517190.1 GI:9741220
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                                                                                                                                                                    Triticum aestivum
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/!ssue_Lype."developing caryopsis (4.-15.DAP)"
/lab_host="XLOLK"
/lab_host="XLOLK"
/lab_host="XLOLK"
/note-"Vector. plasmid pBK CMV, Site_1. Ecckl, Site_2:
Xhol; mkNA was made from developing caryopsis (3.-15.DAF)
of spring karley 'variety' Barke', a high quality malting
variety. Cloning sites: Ecokl (5'-end of cDNA) and Xhol
(3'-end of cDNA). NOTE: Due to a cloning artelact caused
by the kit, in most cases the Ecokl site is NoT present,
as well as the Ecokl adapter. Average insert size is 1 kb
Sequence trimming. Vector sequences and sequence ends were
trimmed from the 5' and 3' end until a 50 bp window.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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Hordoum vulgare chNA clone HY06018V 5', mRNA sequence.
ALS07813
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44.7%; Pred. No. 0.019;
ive 0; Mismatches 349; Indels 3; Gaps
432 outoagermogeurmentalaangeeliggaligaangi gal egaquagaangeel teageer 491
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Contact: Michalek W
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/clone="HY06018V"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL542697 LTI_FL002_FL1 Homo sapiens JENA clone GSODE011YK20 5 prime
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini: Hominidae; Homo.
1 (bases 1 to 1078)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 GGAGAGGTCACGAGGGTACTACAGGGGGGGGGAAGAAGATCTGGGCGAGGTNCATC 508
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                                                                                                                                                                                                                                                                                                                                                                                 709 accaccagcaccetgcaggagragatrgrriggatgaccagcaacccccatcccqtq 768
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                                                                                                                                                                                                     209 TOGGOCCICACTACAAGAAGTACTCCGAAGAGATACCGGGGGCCCAACTACTACTACTACGCGCCAAC 268
                                                                                                                                                                                                                                           589 nagatgetgaaggacaccatcaacgaggacacccgtg 648
                                                                                                                                                                                                                                                                     649 caeyeegyeeecateqeeeceggecagatgegegageecegegggeagegaatrgrrggr 708
                                                                                                                                                                                                                                                                                                                                              329 GACCCCCCCCCCCGCGCGCGCCTCAACGTCTTAACTTCAACTTCGCCAACTTCGCC 388
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                                                    472 gaggagaaqgeetteageeeegaggtgateeeeatgtteaeeqeeetgageg---gge 528
                               412 ggccagatggtgcaccaggccatcagccccgcacctgaacgcctggatgaaggtgatc 471
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29 SUSSANSANGENGERANGERANGGARTERFINGEREGETEGTGGGGGCTGACGCCGNTG 88
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                     Li,W B., Gruber,C., Jessee,J. and Polayes,D
Full-length cDNA libraries and normalization
Unpublished (2001)
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and cloned into the Not I and Eco RV sites of the pCMVSFOKI 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.ccm URL.

http://tulllength.invitrogen.com"

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	AP201927 Synthetic	AF287354 Synthetic	AF202464 Synthetic	AF202465 Synthetic	AP287352 Synthetic	AF287353 Synthetic	AX035453 Sequence	AX056836 Sequence
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	Score	1201	1143.2	1117.8	1117.8	1075.8	1064.2	930.2	930.2
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RMYSPTSILDIPGGPKFPFRYDFYKTLRAEQASQDVKNWMTETLLVONANPDCKT
ILKALGPAATLEEMMTACQGVGGPGHKARVLAEAMSOVTNPATIMMQRGNFRNORKTV
KCFNUGKEGHIAENCEAPPKRGTWPTGFEGHQMKDCTFRQANFIGKIWPSYKGFPGNF
LQSRPEPTAPPEESFRFGEEKTTPSQKQEPIDKELYPLTSLRSLFGNDPSSQ"
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AVNPGLLETSEGCRQTIGQLQPSIQTGSEELRSLYNTVATLYCVHQRIDVKDTKEALE
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Matches 185; Conservative O: Mismatches 140; Indeis 36,
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Submitted (12-JUL-2000) Chemical Pathology, Women's and Children's
Hospital, 72 King William Koad, North Adelaide, SA Sünk, Australia
Location/Qualifiers
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zur Megede,J., Chen,M.C., Doe,B., Schaefer,M., Greer,C.E.,
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/db_xref "G1:7229425"
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VEEKAFSPFVIPMFSALSFGATPQDLNTMLNTVGGHQAAMÜMLKETINEEAAEWDRYH
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RMYSPTSLEDIRQGPKEPPRDYVDRFYKTLRAEQASQDVKNWMTFTLLVQNANPDCKT
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KCFNCGKEGHTARNCRAPRKGCWRCGREGHQMKDCTERQANFLGKIWPSYKGRPGNF
LGSRFEPTAPPEESFPPGFEKTTPSQKQFPTPKELYPLTSTPSLFGNDPSSQ"
Selby,M., Otten,G.R. and Barnett,S.W.
Increased expression and immunogenicity of sequence-modified human
                                                                                                                                                                                                              chiron Corporation, 4560 Horton
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/db_xref-"taxon:32630"
1, .1509
                                                immunodeficiency virus type 1 gag gene
_T__Virol._74 (6), 2628-2635 (2000)
                                                                                                                                                                                                          Submitted (05.Nov 1909) Vaccines,
Street, Emeryville, CA 94608, USA
Location/Qualifiers
                                                                                                                                                                   zur Megede, J. and Barnett, S.W.
Direct Submission
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Bost Local Similarity 85.19
Matches 1299, Conservative
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RCFNGGKEGHTAPNGPAPRKKGGWPGSPGHGMKPGTFPGANFLGKTWPSYKGRPGNF
LGSPPFPTAPPFESFPPGFEKTTPSGKGEFIDKELYPLJSLRSLFGNDPSSQ"
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RTEEEUNESERRAGGAAAAAAASTGNSSGVSGNYPTVGNTGGMVHQATSPPTLNAWVEV
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RMYSPTSTLEDIEGGPKEPFRDYVDREYKTLRAEGASGDVKNWMTETLLVONANDDGKT
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                                                                                                                                                                                                                                                                                  Increased expression and immunodenicity of sequence-modified human immunodeficiency virus type 1 gag gene
J. Virol. 74 (6), 2628-2635 (2000)
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Selby,M., Otten,G R. and Barnett,S.W.
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NPQSQCVVESMNKFLKKIIGOVPPQAFHIKTAVQMAVFIHNFKRKGIGGYSAGERIV
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Fuller, M. and Anson, D.S.
Direct Submission
Submitted (12-JUL-2000) Chemical Pathology, Women's and Children's
Hospital, 72 King William Road, North Adelaide, SA 5006, Australia
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Fuller,M. and Anson, D.S.
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Direct Submission
Submitted (12-JUL-2000) Chemical Pathology, Women's and Children's
Hospital, 72 King William Road, North Adelaide, SA 5006, Australia
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                                                                                                                                                     1072 egegitgeitggeegaaggegaitgageeagge- eeaacagegfigaaeafeafgafgatgeagaa 1128
                                                                                                                                                                                                                              1423 AAGCAGGAGCCGATAGACAAGGAACTGTATCCTTTAACTTGGCTCAGATCACTGTFGGC 1482
952-etgetiggt gragaaegerdaareergaet geaagaerat eet gegegetet eggeeeegge -1011
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| 1198_c | 1285_q 689_t
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Best Local Similarity 77.4%; Pred. No. 4.5e-93;
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Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
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Mitrophanous.K. Kingsman,A T and Kim,N.
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Patint Wo 941397-A 2 19-AUG-1999;
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/organism="synthetic construct"
/db_xret="taxon:82630"
/note "pSYNGP4 - codon optimised HIV-1 qaqpol with 20 bp of the leader sequence of HIV 1, etc"
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0; Mismatches 316; Indels
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1 (bases 1 to 4327)
Uden,M. and Mitrophanous,K.
Anti-viral vectors
Patent: WO 0055341-A 14 21-SEP-2000;
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Matches 1175, Conservative
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/db_xret "taxon-12630"
/db_xret "taxon-12630"
/note="psyNGP3 - codon optimised HIV-1 gagpol with leader sequence from the major splice donor"
sequence 110m the major splice donor"
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Patent: Wo 6055341-A 13 21-SEP-2000;
UDEN MARK (GE); OXFORD RIOMEDICA LID (GB); MITROPHANOUS KYPIACOS
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Sequence 13 from Fatent WG0055341
AX035464
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DEFINITION ACCESSION

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Sequence 12 from Patent W00055341.

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/organism="synthetic construct"

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/note "pSYNGP2 - codon optimised HIV-1 gaqpol with leader

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Novitsky,V.A., Montano,M.A., McLane,M.F., Renjifo,B., Vannbery,F.,
Foley,B.T., Ndung'u,T.P., Rahman,M., Makhema,M.J., Marlink,R. and
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HIV-1 isolate C-96BW05.02 country Botswana, complete genome.
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KEGHIAKNCRAPRKGCWKCGKEGHQMKLOTERGANFFERNIAFEGGEAKEFPFEGIR

ASSPNSTNSPTSRELQVRGDNPPSERAFGGGTLAGTLNCPQITLMQRPLVSIKVGGO

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VGPTPVNITGRNMITGLGCTLNFPISPIETVPVKLKPGMDGPKVKQWTLTEEKIKALT

EICEBMEKEGKITKIGPENPYNTPVFAIKKNSTKWKKLVDFKELNKKIQUFWEVQLG

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IKWGFTTPDKKHQKEPPFLWMGYELHPDKWTVQPIQLPDKDSWTVNDIQKLVGKLNAA

SQIYPGIRVYYDDKLLRGARATTDVVPLTEGAELELAENREILKEPVHGYYYDPSKDL
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GKTPKFRLPIOKETWETWWIDYWOATWIPEWEFVNTPPLVKLWYOLEKEPIPGVETFY
VPGAANRETKLGKAGYVTDRGRQKIVSLTETTNOKTELOAIQLALODSGSEVNIVTDS
OYALGIIQAQPDKSESELVNQIIEQLIQKEWVYLSWVPAHRGIGGNEQVDKKLVSGIR
KMLFLDGIDKAQFEHEKYHNNWRAMADEENLPPIVAKEIVASCDKCQLKGEAIHGOVD
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HTDNGTNFTSAAVKAACWWAGIQQEFGIPYNPQSQGVVESMNKELKKIIGOVRDQAEH
LKTAVQMAVFIHNFKRGGIGGYSAGERIIDIIATDIQTKELQKQIIKIQNFKVYYKD
SRDPIWKGPAKLLWKGEGAVVIQDNSDIKVVPRRKAKIIKDYGKQMAGADCVAGGQDE
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Alnpglibtaegckoimkolopalotgteelkslyntvatlycvhagievrdtkbald
Kiebeonksooktooakeadgkvsonypivonloggwyhqaisprtlnawykviebka
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GPGATLEFMMTACQGVGCPGHKARVLAFAMSQANSVNIMMQKSNFKGPRRNVKCFNCG
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                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (03-DEC-1998) Immunology and Infectious Diseases, Harvard School of Public Health, FXB-310, 651 Huntington Avenue, Boston, MA
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Novitsky, V.A., Montano, M.A., McLane, M.F., Renjifo, B., Vannberg, F.,
Foley, B.T., Ndung'u, T.P., Marlink, R. and Essex, M.
immunodeficiency virus type 1 subtype C a set of 23 full-length
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/protein_id="AAD17072.1"
/db_xre1="G1:4324808"
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/codon_start=1
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/protein_id="AAD17071.1"
/db_xref="GI:4324807"
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/country="Botswana"
/note="subtype: C"
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/gene="vif"
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277. .4589
/gene="pol"
                                                               clones from Botswana
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ELKDRKQEVHALEY REDVVPLGGNNSNEY RELINCNTSATTGACPKVSEDP LPTHYCTE
AGYA ILKCNNQTFNGTGPCNNVSSVOCAHGIKPVVSTOLELLNGSVAKGET I TRSENLT
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Zdb_xr-t-"Gr 4 <24814"

Ztranslation "MKVMSILKNYQQWWMWGILGFWMLJISSVVGNLWVTVYSVPVW

KEAKITLECISLAKAYETEVHNVWATHA/VPTDPNI-QEIVLENVTENENMWENDMVJ-Q
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IVSGFLALAWDDLRSTCLESYHRLRDF11 JAAPVIFLLGGRGWFATRVJGSLVQVWGI
ELKKSAJSLLDTJAJAVAEGTDRJJEFIQRJGRAJRNIPRRJRQGFRAALG"
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ADOLTHMHYFDGFADALTKATTGETVTPPRTYJANHNGVGSLJYLALTALTKPKGPK
PPLPSVRKLVEDRWNKPOKTRGPRONHTMNRH"
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DRIJTRKTRERAEDSGNESDGDLEELSAMVDVGHIRLI.DVNN"
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DRETNNYTDT TYRLLEESQNQQEKNEKDLIALDSWQNLWNWFSITNWLWYIKIFIMIV
                                                                                                                                          /translation-"MENRWQVLIVWQVDRMKIRTWNSLVEHHMHISKAAKGWEYRHHY
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/qene-"env"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       637 GEFGACGGGAAGGFCAGATTATTGTATAGTAGAGGTACAAGGGAAAGGTA 696
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/qene="net"
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1 (bases 1 to 9056)
Novitsky,V.A., Montano,M.A., McLane,M.F., Renjifo,B., Vannberg,F.,
Foley,B.T., Ndung'u,T.P., Rahman,M., Makhema,M.J., Marlink,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C. a set of 23 full length clones from Botswana
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          1021 gaggagatgatgaccgcctgccagggcgtgggcggcccggcccggggcccagaggccgcgcgtgctg 1080
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781 eggtygateateetgggeetgaacaagategtgeggatgtacageeeegtgageateetg 840
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Human immunodeficiency virus type 1
Viruses; Retroid viruses; Retroviridae; Lentivirus, Primate
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                                                                         Submitted (03-DEC-1998) Immunology and Infectious Diseases, Harvard School of Public Health, FXB-310, 651 Huntington Avenue, Boston, MA
               2 (bases 1 to 9056)
Novitsky,V.A., Montano,M.A., McLane,M F , Renjifo,B., Vannberg,F.,
Foley,B.T., Ndung'u,T.P., Marlink,R. and Essex,M.
Direct Submission
                                                                                                                                                          /organism="Human immunodeficiency virus type 1"
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                                                                                                                                                                                                                         /country="Botswana"
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WNSTLQGVSKKLEEHFSKKATKFEPSSGGDLETTTHSFNCRGEFFYCDTSQLFNSTYS
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LVSGPIALAMDDLRSICLFSYHRLRGFILIAARVLELLGGRGMFALKYIGSLVGYWSL
ELKKSAISLLDITATAVAEGIDKITEFIQKICKAIRNIPRRIRGGFEAALQ"
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AGYATLKCNNQTFNGTGPCNNVSSVQCAHGTKPVVSTQLLLNGSLAKGETTTRSENLA
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KOLOTRTLAVERYLKDQQLLGTWGCSGKLJCTTAVPWNSSWSNRSHDEJWDNMTWMQW
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                                                       ZFranslation="Minelakupprigugalivapilaivvwilayieyrklirqeki
GRIJERTRERAEDSGNESDGDIEELSAMVDVGHLRILDVNN"
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637 GPTGAGGGAAGGTPAAPPAAATTAPPPTAFAGTAGAAGAACCTAAAAGGGAAAATGGTA 696
                                               601 accatcaacqaqqaqqerqeqqaqtqqqaecqeetqeacereqtqeaqqeeqqeeeqtq
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VSILDIROGPKEPFRDYVDRFFKTLRAEOATODVKNWMTDTLLVQNANPDCKTILRAL
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PTAPPAEPTAPPAESFRFEGTTPAPKQEPKDREPLTSLKSLFGNDPLFQ"
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PKMIGGIGGFIKVROYDOTPTEICGKKALGTVLVGPTPVNIIGRNMLTQLGCTLNFPI
SPIETVPVKLKPGMDGPKVKQWPLTEEKIKALTAICEEMEKEGKITKIGPENPYNTPV
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GIVIYQYMDDLYVGSDLEIGQHRAKVFELREHILKWGFTTPDKKHOKEPPFLWMGYEL
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FSPEVI PMFTALSEGAT PQDLNTMLNTVGGHQAAMOMLKDTI NEEAAEWDRLHPVHAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-JUL-2000) Medicine, University of Alabama at
Birmingham, 701 19th Street, Scuth, LHRB 641, Birmingham, AL 35294,
                                                                                                                                                                                                                                                                                                                                                                                                                                                lentivirus group.
1 (bases 1 to 9034)
Podenburg,C M , Li,Y , Trask,S.A., Chen,Y., Decker,J.,
Robertson,D.I , Kalish,M L., Shaw,G.M., Allen,S., Hahn,B.H. and
Near full-length clones and reference sequences for subtype C isolates of HIV type 1 from three different continents AIDS Res. Hum. Retioviruses 17 (2), 161-168 (2001)
                                                                                                                                                                                                                                    10.AFR.2001
                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Frimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rodenburg, C.M., Li, Y, Trask, S.A., Chen, Y., Decker, J., Robertson, D.L., Allen, S., Shaw, G.M., Hahn, B.H. and Gao, F. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Human immunodeficiency virus type 1"
                                                                                                                                                                                                               AF286234 9034 bp DNA VRL 1C
HIV-1 strain 98T2013 from Tanzania, complete genome.
AF286234
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/protein_id="AAK31054.1"
                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="98TZ013"
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136. .1635
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TITLE

TITLE

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/LFT. ISTALTON - "MEVPGT PRIMOPHWINGTLGFWTTMTCNVMGNLWVTVYYGVPVW KEAKTTLFCASDAKGYEKEVHINVWATHACVPTDPNPQEIVLDNVTENFNMWKNDMVEQ MHEDIISLWDQSLKPCVKLTPLCVTLNCTNATVTATRNGSDIMNTTSNDGEMKNCSFN 1TTELKDKRQKVSALFYKLDIVPLNKNNNSFGEYRLINCNTSTITQACPKVSFDPIPI
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Dwlikriberaedsgnesegyteelatmvdmghlrlldnndl"
5579. .8170
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                                                              TWIPEWEFVNTFPLVKLWYÇLEKEFIAGARETYYVDGAANRESKIGKAGY TÜPEYÇEKITLAGAETYYVDGAANRESKIGKAGY TÜPRGRÜKI ITLAETTNQKAELQAIQLALQDSGSKVNIATDSQYALGI IQAQPDKSESELVSÜKI LIGKERVYLSWVPAHKGIGGNEQVDKLVSSGIRKVLFLDGIDKAQEEHEKYHSNWRAM ASEFNLPPIVAKEIVASCDKCQLKGEAIHGQVDCSPGIWQLDCTHLEGKI ILVAVHVA SGY IEAEVI PAETGQETA"
                                                                                                                                                                                                                                                                                                                                                                                                                /Lranslation-"MENRWQVLIVWQVDRMKIKTWHSLVKYHMYISRRASGWFYRHHY /Lranslation-"MENRWQVLIVWQVDRMKIKTWHSLVKYHMYISRRASGWFYRHHY BSRHPKVSSEVHIPLGGARLVITTYWGLQTGEGDWHLGHGVSIEWRLKRYSTQVDPSL ADQLIHMHYFDCFADSAIRKAILGHTVIPRCDYQAGHNKVGSLQYLALTALIKPKRRK PPLPSVRKLVEDRWNNPQKTRGRRGNHTMSGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rransiation="MEQPPEDQGPQREPYNEWALEILEDLKQEAVRHFPRPWLHDLGQ
                           VPLITKEAELELLEENKETLIKEPVHGVYYDPSKDLIAEJŲKÕGÕIÕWTYQIYQEPFKNLK
TGKYAKMRSAHTNDVKQLTEAIQKIAMESIVIWGKTPKFRLPIQKETWETWWTDYWQA
HPDKWTVQP1QLPEKDSWTVND1QKL/VGKLNWASQ1HSG1K1RQLCKLLRGAKALTD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Join(5312, .5387,7733, .7980)
/gene="rev"
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/gene="tat"
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/product="rev protein"
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/gene="vpr"
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                                                                                                                                                                                                                                                                     4384. .4962
/gene="vif"
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/gene="vif"
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/gene="vpr"
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856_CAGGAACAATAGCATGGATGACAGGTAACCCACCTCTTCCAGTGGGAGACATCTATAAA 915

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DKYGAFTTSNTVATNADLAWLEAQEEEEEVGFPVRPQVPI PPMTYKAAFNI SFFTŘEK
GGLEGLIYSKKKODILDGWYHTQGFFPDWQNYTPGPGVKYPLTFGWCFKLVPVDPRE
VEEANKGENNTTHPMSQHGMEDEDPFVLPWEFDSSLAPPHLAPEKHPEYYFDC"
1622 c. 2165 g. 1961 t.
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                                                                 SENTTONAKT FIVHUNESVETMCTRPGNNTRK SVR I GPGQTFFYTND FIGDI RQAYON I
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Pred, No. 1.9e-74;
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/db_xret-"GI.13569326"
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Š 3 601-arral caucquqqaqqccqccquqt qqqacqcct qcaccccqt gcaqqccqqqcccqttq-660 7.46 ACCATCAALGAGGAGGCTGCGGAAFGGGATAGATTACATCCAGTGCAGGGGCCTATA 795 661 generaggeragalgegandengagenengegagegagegategengegegeeaeeageaeeetg 720 721 huggaghagathgentggatgannaghaannnoncentgtgnngtggggaeatetaeaag 780

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1081 geoggaggegatgageeraggeogaaeagegtgaaeateatgatgetgeagagageaaetteaag 1140
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901 etgegegregageaggeearceaggaegtgaagtgaagttgatgatgaeggageettgetgg1960
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August 8, 2001, 18:25:01 ; Scarch time 252.53 Seconds (without alignments) 3677.450 Million cell updates/sec Вип си:

US-09-475-704-3 1479

..andanonnotgagonagtaa 1479 1 atgqqqqqqqqqqat Perfect services - Journal boy

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1460202 Total number of hits satistying chosen parameters:

730101 seqs, 313950809 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries ¥00! Post-processing: Minimum Match 0% Maximum Match 100

Database :

N_Geneseq_0601:* 1: __cqn1_4/qcqdata_qoneseq_qeneseqn_NA1980_DAT.* 2. __cqn1_4/qcqdata_qqeneseq_qqeneseqn_NA1981_DAT.* 3: __cqn1_4/qcqdata_qqeneseqn_NA1982_DAT:* 4: __cqn1_4/qcqdata_qqeneseq_qqeneseqn_NA1983_DAT:*

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/cqul_9/dcqdata/qeneseq/qeneseqn/NA1998.DAT:* Zequi 9/gegdata/geneseq/geneseqn/NA1999 hAT.* 9/40/9data/4PDPSP4J/4PDPSP4j/NA2666 1AI * /cgn1_9/qcqdata/geneseq/geneseqn/NAZ001.DAT:* Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by apalysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Seore		Ouery Match Length DB	H.	110	Description
	1479	1479 100.0	1474	2	AAA51609	HIV Synthetic Gan
1	146.3	5.85		៊	AAA51625	HIV codo; cpt jmj.ee
-	1275.8	86.3	1509	7.1	AAA51610	HIV synthetic Gad
4	1260.B	71 60 60	6051	<u>:</u>	AAA51626	HIV codon optimize
<u>.</u> ~	1197.8		,	2.1	AAA70412	Synthetic HIV Gad
£	1197.8		`	<u>.</u>	AAA70472	HIV bicistronic co
7	1197.8		,	2.1	AAA70473	HIV bicistronic co
x	1197.8		,	2.1	AAA70471	HIV bicistronic co
5	1197.8	81.0	4766	21	AAA70470	HIV bicistronic co
10	1145.8		•	2.1	AAA70415	Synthetic HIV Gag/
=	1114.6		1853	2.1	AAA70413	HIV Gay-protease e

99WO · US31273.

90 DEC 1999;

06 JUL 2000.

WC200019304-A2.

99US 0152195. 98US-0114495.

31-DEC-1998; 01 SEP 1999;

(CHIR) CHIRON CORP.

HIV Gag-protease e HIV Gag-protease e HIV Gag-polymerase Codon optimised Hu Packaging construc HIV Gag common req Humanised EIV-1 ga	Synthetic 11V day HIV gagpol-SYNGP of Human immunodefich Nucleotide sequenc HIV partial leader HIV partial leader HIV complete leader Humanised HIV-1 qa	HIV-1 non-subtype HIV-1 non-subtype HIV-1 non-subtype Complete sequence Entire sequence HIV-1 non-subtype HIV-1 non-subtype HIV-1 non-subtype	HIV-1 non-Subtype daup HIV wild type daup Human immunodetici Nucleotide segmenc Human immunodetici Attenuated HIV-1 s Sequence of LAV vi pHIV32 tragment co Insert region of v
AAA70475 AAA70476 AAA70414 AAZ52051 AAZ52055 AAA70417		<	1 AAF57923 0 AA208722 1 AAA3371 2 AAC80875 2 AAT14180 AAN60365 6 AAT04701 6 AAV58244
1865 21 1865 21 4319 21 1503 21 1268 21 1353 22	44444444444444444444444444444444444444	89960 21 8992 21 8972 21 9143 11 9236 9 8953 21 89193 20	8966 21 4307 20 4307 21 4307 21 4307 22 9181 22 9718 17 9193 7 3808 19
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ALIGNMENTS

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/product. Synthetic_Gaq
/note= "Codon usage pattern was modified and inhibitory
elements (INS) and RRE sites were inactivated
resulting in improved expression"
                                                                                                Sag, expression cassette, antigenie, type C. HIV, Eng, synthetic;
                                                                                                         ENA immunization, packaging cell line; antiqen presentation, ss.
                                                                                                                             Ruman immunodeficiency virus type C strain AF110965.
                                                                                                                                                            Location/Qualitiers
                                                                              HIV synthetic Gag polynucleotide.
                   AAA51609 standard, DNA; 1479 BP
                                                          (tirst entry)
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                                                          41-00T-2000
                                                                                                                                        Synthetic.
                                        AAA51609;
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           AAA51609
RESULT
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Expression cassettes comprising a polynucleotide encoding autigenic type c human immunodeficiency virus (HIV) Gag or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and production of Gag- and/or Env-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540
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                                                                                            Polynucleotide encoding antigenic type C HIV Gag polypeptide of a HIV Env polypeptide and the polypeptide useful for immunizing a mammal
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                                                                                                                                                                                                                                                                                                                                              associated to the immune system of the host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Mismatches
                                                                                                                                                                       Claim 2; Page 92-93; 113pp; English.
                                                                                                                                   especially human against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 1479, Conservative
               Zur Megede J;
                                               WPI; 2000-452401/39.
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                                                                 Р-РЅ⊔Н; ААҮ96943.
               Barnett S,
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                                             bbl atogeceeeggeeagalgegegageeageeeeg
                                                                                    721 etgeuggayeayateyeetggatgaeeageaarrinnnnatrinnigtgggeganatetae
                                                                                                                          721 etgeaggageagategeetggatgaenageaanneenateeegtgggegaeatetae
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                                                                                                        Human immunodeficiency virus type C strain AF110965.
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production of Gaq- and/or Env-containing proteins, Synthetic Env and Gaq expression cassettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antiqen entrapped or associated to the immune system of the host.
                                                                                                                                                                                                                                                                                                                                                                             Expression cassettes comprising a polynucleotide encoding antigenic type C human immunodeficiency virus (HIV) Gag or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and
                                                                                                                                                                                                                                                                      Polynucleotide encoding antiqenic type C HIV Gag polypeptide or a B
Env polypeptide and the polypeptide useful for immunizing a mammal
especially buman against HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1479 RP; 325 A; 533 C; 461 G; 160 T; 0 other;
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                                                                       99W0-US31273.
                                                                                                        98US-0114495
                                                                                                                            99US-0152195
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                                                                                                                                                              (CHIR.) CHIRON CORP.
                                                                                                                                                                                                                                     WPI: 2900 452401/34
WO200039304 AZ.
                                                                      30 DEC-1999;
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98.98; Score 1463; DB 21; Length 1479;
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0; Mismatches 10;
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                                          expression cassette; antigenic; type C; HIV; Env; synthetic,
                                                              DNA immunization; packaging cell line; antigen presentation, SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1509 BP, 320 A, 556 C, 472 G, 161 I, 0 other;
                                                                                             Human immunodeficiency virus type C strain AF110967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 93; 113pp; English.
            HIV synthetic Gag polynucleotide
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99US-0152195
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Query Match 86.3%; Score 1276.8; PB 21; Length 1509; Best Local Similarity 92.5%; Pred. No. 1.4e-160; Matches 1399; Conservative 0; Mismatches 77; Indels 36; 0
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expression cassettes exhibit increased potency for induction of cytotoxic T-lympsocyte (CTL) responses by DNA immunitation. Gag of HIV-1 self-assemble into non-infectious virus like particles which are used as a matrix for the proper presentation of an antiqen entrapped or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production of Gag- and/or Env-containing proteins. Synthetic Env and Gag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide encoding antiqenic type C HIV Gag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially bacan against HIV
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                                                                                                                                                                                                                                                                                                          DNA immunization; packaging cell line; antigen presentation; ss
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                                                                                                                                                                                                                                                                                                                                                Human immunodeticiency virus type C strain AF110967.
                                                                                                                                                                                                                                                  HIV codon-optimized synthetic Gag polynucleotide.
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The present sequence is the coding sequence of a HIV Gag expression cassette, Gag.ModSF2. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV
                                            1378 ececegeogagagetteegettegaggagaccaccecgececaagcaggageccaag 1437
                                                                                                                                            1420 g-----aecgegagaceetgaecageetgaagagetgtaggeaacgaeee 1467
                                                                                                                                                            1258 aaggantgnachgagngnnaggnnaacttnntgggnaagatotggcoocoocoocoocaagggc 1317
                            Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic HIV Gag expression cassette coding sequence Gag.ModSF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hartog K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection and acquired immunodeficiency syndrome (AIDS).
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                                                                                                                                                                                                                                                                                                                                                                                                                        HIV-1; AIDS; Gag; vaccine; expression cassette; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zur Megede J, Srivastava I, Lian Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                           AAA70412 standard; DNA; 1515 BP
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                                                                                                                                                                                                                                      1498 ctgagccagtaa 1509
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81.0%; Score 1197.8; DB 21; Length 1515; 89.3%; Pred. No. 3 5e-156;

Indels

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Similarity

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1009 eccygogecaycetygaggagatgatgaccgcetgccagggcgtgggggggggccccagccac 1068
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                                                                                           67 ctgcgccccggcggcaagaagaagtacaagctgaagcacatcgtgtgggccaqccgcgag 126
                                                                                                                                121 etggagaagttegeeetgaareregerigriggayaceayegaggetgeaageagate 180
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The present invention relates to synthetic HIV Gaq and Env expression cassettes. The Gaq protein of HIV is needed for the assembly of virus-like particles. In addition, the Gaq protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The
                                 1183 ggccanatogonognaantgongonononognaagaagggn gotggaagtgoggeaag 1242
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                                                                   1147 coapogogadenticoacaacaacagaaagaacagtoaagtacticaactgoggaaagaa 1206
                                                                                                                                                                            1243 yayyqddanyayatgaaqqantgaccqaycqonaqqqaqttoctqqqqaaaqatctqq 1302
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                                                                                                                                                                                             Hartog K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV bicistronic construct qp160.modUS4.de1V1/V2.Gag.modSF2.
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                                                                                                                         Lian Y,
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Walker C;
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expression cassettes may be used for the recombinant expression of HIV Gag- and Env-polypeptides which may then be used to vaccinate against HIV
                                                                                          expression cassettes of the present invention. This construct is
bicistronic in that the coding sequences for Env and Gag are under the
centrel of a single CMV premoter and between the two coding sequences an
                                              infection and acquired immunodeliciency syndrome (AIDS). The present sequence is a synthetic construct constructed in the generation of the
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                                                                                                                                                                                                                                                                                Score 1197,8, 198
Pred, No. 3e-150;
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89.38;
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HIV bicistronic construct gp160.modSF162.dolV2 Gag modSF2.
                                                                                                                                 HIV-1; AIDS; Gag; vaccine; expression cassette;
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 28-NOV-2000 (first entry)
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Gag-and Env-polypeptides which may then be used to vaccinate against HIV Gag-and Env-polypeptides which may then be used to vaccinate against HIV sequence is a synthetic construct constructed in the generation of the expression cassettes of the present invention. This construct is bicistronic in that the coding sequences for Env and Gag are under the control of a single CMV promoter and between the two coding sequences an Internal Ribosome Entry Site (IRES) is present.
                                                                                                                                                                                                                                                   The present invention relates to synthetic HIV Gag and Env expression cassettes. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassettes may be used for the recombinant expression of HIV.
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            Liu H;
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Greer C, Selby M, Walker C;
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Pred. No. 3e-150;
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89,38;
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The present invention relates to synthetic HIV Gaq and Env expression cassettes. The Gaq protein of HIV is needed for the assembly of virus-like particles. In addition, the Gaq protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassettes may be used for the recombinant expression of HIV Gaq- and Env-polypeptides which may then be used to vaccinate against HIV infection and acquired immanuabliciency syndrome (ALDS). The present sequence is a synthetic construct constructed in the generation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression cassettes of the present invention. This construct is bicistronic in that the coding sequences for Env and Gaq are under the control of a single CMV promoter and between the two coding sequences an Internal Pibeseme Entry Site (IRES) is present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expression cassettes encoding the human immunodeficiency virus (HIV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tor vaccinating against BIV
                                                                                                                                                                                                                                                                                                                                                                                      Zur Megede J, Srivastava I, Lian Y, Hartog K,
elby M, Walker C;
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0, Mismatches 132, indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gay containing polypeptide users, for vaccinating agains infections and acquired immunodeficiency syndrome (AIDS)
                                     HIV-1; AlbS; Gaq; vaccine; expression cassette; Env; ss
HIV bicistronic construct gp160.modUSF162.Gaq.modSF2.
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Chimeric - Human immunodeficiency virus type 1.
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Matches 1347, Conservative
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The present invention relates to synthetic HIV Gag and Env expression cassettes. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The expression cassettes may be used for the recombinant expression of HIV Gag- and Env-polypeptides which may then be used to vaccinate against HIV infertion and acquired immunodeficiency syndrome (AIDS). The present sequence is a synthetic constructed in the generation of the expression cassettes of the present invention. This construct is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.3%; Pred. No. 3e-150;
Matches 1347; Conservative 0; Mismatches 132; Indels 30;
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Selby M, Walker C;
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                                                                                                                                                                                                                                                                                                                                           HIV-1; AIDS; Gag; vaccine; expression cassette; Env; ss.
                                                                                                                                                                                                                                                                                                            HIV biristronic construct gp160.modUS4.Gag.modSF2.
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                                                                                                                                                                                                    AAA70470 standard; DNA; 4766 BP.
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The present sequence is a HIV GaqZHepatitis C virus (HCV) core fusion coding sequence. The Gaq protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and early post-entry steps in viral replication. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to synthetic HIV Gag expression cassettes. The present sequence was cloned and used to generate the expression cassettes
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                                                                                                                                                                                                                                                                                             1303 cecagecacauquqeeqeeccqgcaartteetqeaggeaqeeqeeee 1362
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                                                                        1243 gagggeeaeragalgaaggaetgeaeegagegeeaggeaaetteetgggaagatetgg
                                                                                                                                                                                   4553 eccagetacaagggeegeecogacactteetgeagageereceggeeeeg
                                                                                                                                                                   Gag-containing polypeptide useful for vaccinating against HIV infections and acquired immunodeficiency syndrome (AIDS) -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic HIV Gag/HCV core fusion coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA70415 standard; DNA; 2031 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                             247 accgiggccacccigiacigcgigcaccagegeateyaegicaaaggacaccaaggaggec 306
                                                                                                                                                                                                        121 ctyqaqaagtteqeeetgaaceeeggeetgetgqaqaeeagegagqgetgeaageagate 180\,
                                                                                                                                                                                          61 elgegeceggeggeaagaagtgetacatgatgaagearetggtgigggecageegegag 120
                                                                                                                                                                                                                                                                                 127 ctggagcgcttcgccgtgaaccccggcctgctggagaccagcgagggctgccgccagatc 186
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        24.1
        accqtqqcqtqcacqaqaaqaaqtccqcqaqacaccaaqqaqqcc

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                                                                                                                                                                                                                                                                                                                181 attergresagetycaceeegeeetycagaeegggsagegagggetgaagageetgteaae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132; Indels
                        Sequence 2041 BP; 421 A; 707 C; 645 G; 257 T; 0 other;
                                                                                    2e-150;
                                                                     ЭB
                                                                                                  0; Mismatches
                                                                   80.9%; Score 1195.8;
89.3%; Pred No 6.20
                                                                        Query Match
Best Local Similarity 89.33
Matches 1345; Conservative
(AIDS).
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1363 ecegeegaagagetteegette----qaagaaceaeceeeggeeagaageagag--- 1413
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                                                                                                                                                                                                                                                                                                    1267 gagggccaccagatgaaggactgcaccgagcgccaggccaacttcctgggcaagatctgg 1326
                                                                                                                                                                                                                                                                                                                                                          1327 eccagetacaaggyeegeeeeggeaaetteetgeagageegeeegggeeeaeegeeee 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1447 ategacaaggagetgtaeeeeetgaeeageetgegeageetgteeggeaaegaeeeeage 1506
                                                                                                                                                                                                                    1207 ggccacaccccaggaactgcrgrgrrrrrgraagaagggctgctggcqctgcggccgc 1266
                                                                                                                                                                                                                                                                                                                                creaqeeacaagggeeqeeeeggraaetteetgeagageegeeeegageeeacegeeere 1362
qacaccotgotggtgcagaangnnaannnngantgnaagaccatootgogoqototoggo 1008
                           967. gugubbobtgotggtbgbaggapppaannnngantgnaaganpatnetgaaggntntoqqn 1026
                                                      1069 aaggeeegegtgetggeegaggegatgageeaaggeeaaca----eeageetgatgatg 1122
                                                                                                                                      1087 aaggeeegegtgetggeegaggegatgageeayytyaeyaaeeeggegaeeateatgatg 1146
                                                                                                                                                                 Expression cassettes encoding the human immunodeficiency virus (HIV)
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                                                                                                                                                                              HIV Gag-profease expression cassette coding sequence GagProt.ModS
                                                                                  cocycoyocacottyyaygayatyatyanogeotyonayyyoqtyyygogynoono
                                                                     Hartog K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV-1, AIDS, Gag-protease; vaccine; expression cassette; ss
                                                                                                                                                                                                                                                                                            Lian Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ede J, Srivastava I,
Walker C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1.
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The present sequence is the coding sequence of a HIV Gag-protease expression cassette, GagProt.ModS. The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in man, stages of the HIV life cycle, including assembly, it is maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate
                                                                                                                                                                                                                                                                                                                       against HIV infection and acquired immunodeficiency syndrome (ALDS).
Jaq-rontaining polypeptide useful for vaccinating against HIV
                        intections and acquired immunodeficiency syndrome (AIDS)
                                                                           Maim 5; Fig 7; 491pp; English.
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Sequence 1853 BP; 421 A; 624 C; \$80 S; 228 T; 0 other;

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61. etgegeseeggeggaagaagtgetaratgatgaagearetggtgtgggeeageeggggg-120
                                                                                                                                                                                                               12) is tayaganatts good tyaasoooniy agiictactagadaccaaagaagagatacaaagaata (180
                                                                                                                                                                                                                               807 ctygagaugategaggaggaggagaacaggteeaagaagaaggeegee 366
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161. greg - - - - - - - acaagggcaaggtgageeagaaetaeceategtgeagaaeetg - 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 nagggg ugalgglannanggreatrags eregrarertyaaggreggggggggggggg 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        529 yn ar che eaddan Fgaaracyatyt fyaar abryt gggegggegegegegtg 588
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                                                                                                                                                                           67 intgryerreggeggraaggaagaagtacaagetgaagraratingtgtgggecagengag 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 gengenggnagnagnagnagnagnagnagnagnagnagnanereatrgtgeagaanetg 426
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                                                                     [B] at regerager geaer regener (gradareganagegaggagger) gaagagnet gt. Leaa e
                                                                                                                                                                                                                                                                                                                                                        241 - accept queceaccet qt act.gcgt geargagaagat egaggt eeggegaeereaaggaagge
                                                                                                                                                                                                                                                                                                                                                                                                                          801 etggaeaagategaggaggaggagaaaagtgecagcaggaggecgaggec
                                                                                                                                                                                                                                                                                                                  75.4%; Score 1114.6; DB 21; Length 1853;
85.8%; Pred. No. 3e-139;
Live 0; Mismatches 184; Indels 30; O
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Matches 1295; Conservative
  Query Match
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HIV Gag professe expression cassette coding sequence GagProtMod.SU2(GPL).
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                                                                                                                                                                                                                                                                                                                                                                                                                              1123 s agaagagoanottoaagagos oscagogalogis aagaactis daastacga aaagaa - 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1183 - ggeeacat eggeegeaact geegegeeact and 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1243 gagggeeaeragatgaaggaetgeaergagegeeragggeraartteetgggeaagatetgg 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1267 qaaqqacaccaaatqadaqattqcactqaqaqaqaqaqaqqatttttttaqqqqaqaqatctqq 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1303 creagreacaaqqqeeqereperqqraartiretgraqaqeeqereeqaqereacareqeere 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1447 ataqueadyqaantqtatootttuacttoontgagatoactettiyynaanyanoviteg 1506
                                                                                                                                                                                                                                                                                   1009 - deeggegenaanetigaagaagatgatganegeet geeagagest aggeggeeeeagenae - 1068
                                                                                                                                                                                                                                                                                                                      1027 ceegeggreaceetggaagagatgatgaeegertgeeaaggeettggeggeereggeerae 1086
                                                                                                                                                                                                                                                                                                                                                         1069. aaggeeegegtgettggeegagggatgageeaggeeaasearriineneagegtgatgatg 1122
                                                                                                                                                                                                                                                                                                                                                                                           1087 aaggeeegeglgetageegageegalgageeaagtgaetgaeegaaceggeeeatealgalg 1146
                                                                                                                                                                                                              949. gasabert getagt graguarynsaan nergan 1 grangalent eet gegeget et egger | 1008
                                                                                                                                                                                                                                                967. gagaccel yetaqi qeaqaaqecaaceeeqaatigeaaqaeeai eei qaaqqei ei egge - 1026
                                                                                                                                        769. iggegaeat chaeaageggiugai earcet gageet gaacaagai egigegaai gi acage 1828
                                                                    829. cooqiqaqcatootqqaqatoaaqoaqqqeoooqaaqqaqoooticoqqaataoqtqqao
                                                                                                      847 secadinayouts et gganatin ginaggan in aaggagen tit si gegaetaegt ggan
                                                                                      HIV-1; AIDS: Gag-protease; vaccine, expression cassette; SS.
                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
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                                                                                         (first entry)
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99WO-US 11245.

40-DEC-1999;

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the present sequence is the coding sequence of a HIV Gag protease expression cassette, GagProtMod.SF2 (GP1). The Gag protein of HIV is needed for the assembly of virus-like paiticles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, viriou maturation after particle release and early post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV infection and acquired immunodeficiency syndrome
                                                                                                                                                                                                 Expression cassettes encoding the human immunodeficiency virus (HIV) Gag-containing polypeptide useful for vaccinating against HIV
                                                                                                           Hartog K,
                                                                                                                                                                                                                                         infections and acquired immunodeficiency syndrome (AIDS)
                                                                                                        , Zur Megede J, Srivastava I, Lian Y, Seiby M, Walker C,
                                                                                                                                                                                                                                                                              Claim 5, Fig 69, 39ipp, English.
               98US-0114495
                                   99US-0168471
                                                                                                                                                                  WPI; 2000-452400/39.
                                                                     (CHIR.) CHIRON CORP.
               31-DEC-1998;
                                   01-DEC-1999;
                                                                                                           Barnett S,
Greer C, 3
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75,4%, Score 1114.6, DB 21, Length 1865, 85.8%; Pred. No. 3e-139; Sequence 1865 BF, 424 A; 627 C, 583 G; 231 T, 0 other, Best Local Similarity Query Match

61 styracorogogyaaagaagtyotaratyatgatyaagraartyyttyytyytyytyoogoogoogoogo 12073 etgegeeceggeggeageagaagtacaagetgaageacategtgtgggeeageegegag 132 ctggagaagttogcoctgaacocoggeotggotggacoagogagggotgcaagcagatc 180 |||||||| 133 etggaqegettegeegtgaaeeeeggeetgetggagaaeeagegaggetgeegeeagate 192 181 alcogecagetgeaeceegeeelgeagaeeggeagegaggaggagetgaagageelgtleaae 240 241 accytggccaccetgtaetgegtgeaegagaagategaggteegegaearareaaggagee 300 253 accqtggccaccctytactycytycaccayegeatcyācytcaaggacaccaaggaggcc 312 etggacaagategaggaggageagaacaagtgecagcagaagatecaqeeggeegaggee 360 1 algygogocoycycoagoaloctgogoggoggoaaqetggacgcctgggagogoalcogc 60 193 etgggceagetgeageeeageetgeagaeeygeagaeagaegagagetgeageagetgtacaae 0; Mismatches 184; Indels Matches 1295; Conservative QQ qn qq QQ QY qu 22 5 δ õ

469 atogaggaggaggeotteageocegaggtgatececatgtteacegeeetgageggge 528 493 gtygaggagaaggcettcagccccgaggtgatccccatgttcagcgccctgagcgagggc 552 gecy-----acaagggcaaggtgagccagaartacccatcgtgcagaactg 408 373 geogeoggeaeoggeaaeageageaggtgageeagaaetaeeeeategtgeagaaeetg 432 cagggecagatggtgcaccaggccatcagccccgcacretgaacgcctgggtgaaggtg 468 361 Db qq Ωp ò $\overline{\mathbf{q}}$ ΟY ΟÝ

1009 eccygegecaycetygaagaagatgatgaeeqeetqeeagggegtggggeggeereageeae 1068 1093 aaggeeegegtgetggeegaggegatgageeaggtgaegaaeeeggegaeeateatgatg 1152 1123 cagaaqaqcaacttcaaqqqqqqqqqqqqqqtqtcaaqtqcttcaaqtqqqqqaaqqaq 1182 1213 ggocacacococaggaactgoogocococococagaaqgactgotggcgctgcggccqc 1272 1502 1303 eccagecacaagggeegeeeggeaetteetgeaydgeegeeeegageeea 1362 1393 ccagaagagagetteaggtttggggaggaaaaaaaacteeeteteagaageaggageeg 1452 1414 ---agcaaggaeegegagaeetgaeeageetgaagaetgageetgtteggeaaegaarenerig 1470 1033 cccgcggccacctggaggagatgatgaccgcctgccaggggggtggggggrcarroggrcar 1092 1153 cagegogycaacttochcaaccaynqqaaqanngloaaqtqriicaactgegqcaaqgag 1212 1183 ggecacateqeeegcaaetqeegegeeeecgeaagaayggetgggaagtgeggeaag 1242 1453 atagacaaggaactgtateetttaaetteeeteagateaetetttggeaaegaeeeteg 1512 949 gacaccetyctggtgcagaacyccaaccecgaetycaagaccatectgegegetetegge 1008 853 couscageatectgganatengagenniaggenniaaggagenttengegantandtggan 912 613 cagaigetgaaggaecateaaegaggeegeegagtgggaeegegtgeaeeeqig 672 709 accaccagcaccetgcaggagcagatrgrefgga†qannagnaannnnoratceeeqtq 768 1243 gagggccaccagatqaagqaetgcaccgaqcqccaqqqccaactfcctggqcaaqatctqgccagcgtgatgatg 589 cagatgotgaaggacaccatcaacgaggaggacgccgagtgggaccgcgfgrannorgfg 649 cacgeeggeeceategeeeceggeenagatgegegageeegeggeageaategeegge 913 egettetaeuugummi grigegrit ja graqqimagimagaang gaaqaantaaat qaar 673 cargreygninalingeniningginagatgragagagaacccgcgcggcagcgacutcgccggc AAA70476 standard; DNA; 1865 BP (firs* ontry) 1471 ageceagtaa 1479 1513 tcacagtaa 1521 00002-ACN 80 13 AAA70476 QQ ΩįΩ op ò QQ q δ ö Db ò ŏ 급 0产 Qγ qq ō 2 ö 2 ò; 5 \ddot{c}

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HTV Gaq-projects expression cassette ending sequence GagprofMod.SF2(GP2).
                                                                                                                                Liu H:
                                                                                                                              Barnett S. Zur Megede J. Srivastava I. Lian Y. Hartog K.
             HIV-1; AIDS; Gag-protease; Vaccine; expression massette; ss
                            Human immunodeficiency virus type 1.
                                                                                           98US 0114495.
                                                                              99WO-US31245.
                                                                                                   9905 0168471.
                                                                                                                (CHIR ) CHIRON CORP.
                                                 WOZO00 49 402 AZ.
                                                                                           41 DEC-1998;
01 DEC-1999;
                                                                             40 DEC 1999;
                                                               96 JUL 2900.
                                    Synthetic
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Expression cassettes encoding the human immunodeficiency virus (HIV) dag-containing polypeptide useful for vaccinating against HIV intections and acquired immunodeficiency syndrome (AIDS) -Claim 5; Fig 70; 391pp; English

Selby M, Walker C;

dreer C,

WPI; 2000-452400/39.

The present sequence is the ending sequence of a HIV Gag-protease expression cassette, GagprotMod.SF2(GF2). The Gag protein of HIV is needed for the assembly of virus-like particles. In addition, the Gag protein is involved in many stages of the HIV life cycle, including assembly, virion maturation after particle release and carly post-entry steps in viral replication. The expression cassette may be used for the recombinant expression of HIV Gag-polypeptides which may then be used to vaccinate against HIV intection and acquired immunodeficiency syndrome. (NIDS).

Sequence 1865 BP; 460 A; 583 C; 569 G; 253 T; 0 other;

4 [8] atcogradatignarycogeretigeagaeeggeageageageagetigaagacetetteaae 240 24) acceptage acceptable of gracify of gracify and additional gracing additional gracing and additional gracing and additional gracing and additional gracing and additional gracing and additional gracing and additional gracing and additional gracing and additional gracing and additional gracing and additional gracing and additional gracing and additional gracing and additional gracing and additional gracing and additional gracing and additional gracing additional gracing and additional gracing and additional gracing and additional gracing additional gracing and additional gracing additional gracing additional gracing and additional gracing additional gracing additional gracing additional gracing additional gracing additional gracing additional gracing and additional gracing additional gracing additional gracing additional gracing additional gracing additional gracing additional gracing additional gracing additional gracing additional gracing additiona 73 etterereregerageaagaagtaraagetgaagetgaageategtgtgggeeageegegag 132 12) chqqaqaaqtteqeretqaaeeeqgeetqetqqaqaaeeaqqetqeaaqcaqate 180 l atgggrgracgracharatertargegaggaagriggangeriggaggaggaisege 60 75.4%; Score 1114.6; DB 21; Length 1865; 85.8%; Pred. No. 3e-139; tive 0; Mismatches 184; Indels Best Local Similarity 85.83 Matches 1295, Conservative 461 geog-Oderry Match 2 Š 3 5 1 5 2 5 = ŝ

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Oy Dib	589 c	589-caqatqcitqaaqqacaccatcaacqaqqaaqqcqqqqqqqqqq	672
άγ	649 0	Paegeeggeeceat egeeeeeggeeagat gegegageeeegggeagegaaat egeegge 	7.08
Cy Siè	709 c	accaeccageaecet geaggageagategeet ggat gae cageaece eecat ee cegtig 	768
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da Pb	949	jacacecty, tyytycayaacyccaacecyactycaayaccateetyggetetegge 	1008 1032
QY	1009 6	scoggogeceageet ggaggagaldaltgaees, et geeaggge glaggeggeeeeeageea 	1068 1092
Oy Db	1069 5 	aaggeeergegtgert ggeegaagegat gageeaggeeaara eeragegtgatgatu 	1122
Qy Db	1123 c	saqaaqqqaaqttcaaqqqqqqqqqqqqqtcaaqtqqqqqqaqqqqqqqq	1182
Ay G	1183 c	ggccacategeregeaactgeegraceereegeaagaaggetgetgaaatgeggraag 	1242
qu equ	1243 J	qaqqarcaccaqalgaaqqastqrascqaqcaccaqqrcaastforlyqqraaqatetqq 	1300 1332
UY Db	1303 0	occayceacaayygeeyeeeqqeaartteefycayageeqeeeegageeeee }	1362 1392
da Oy	1363 c	regecgagagetteegettegaggag areaee eeggeeagaaggag 	1413
Qy	1414	agraaggaccgcgagacctgaccagcctgaagagcctgttcggcaacgaccctg 	1470 1512

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                                                                                                                                                                                                                           HIV Gag-polymerase expression cassette coding sequence GagPri ModSF
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0; Mismatches 184; Indels
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                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1.
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                                                                                                                      AAA70414 standard; DNA; 4319 BP
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Matches 1295; Conservative
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1609 cccggcgccagcctagaagaatgatgaccgcctgccagggcgtgggggggcccagccar 1068
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187 etgggecagetgeagereageetgeagaceggeagegaggaggaggrigegeagerigtacaae 246
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comprising the coding sequence for a beterologous envelope protein and a third retroxinal nucleotide sequence comprising a DNA sequence of interest and lentivirus, preferably HIV, cis acting sequences required for packaging, reverse transcription and integration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the patent discloses new packaging cell line for producing a viral accessory protein independent lentivirus, preferably buman immunodeficiency virus (HIV), derived retroviral vector particles. The packaging cell line comprises a mammalian cell, a retroviral DNA comprising a coding sequence for a letticitis, preferably HIV, gagpel, where the coding sequence has been mutagenised to improve expression of the viral gagpol proteins, a second retroviral nucleotide sequence
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                                                                                                                                                HIV: qaq: packaging cell line; lentivirus; retroviral vector particle;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pol; gene therapy; gene replacement; vaccine; biochemical reagent; codon optimisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                  Codon optimised Human immunodeficiency virus gag coding region.
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11-1-11111111-1-11-1-1111
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                        therapy or gene replacement with improved safety. They can also be used in the development and production of vaccines and biochemical reagents.
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                                                                                                                                                                                                                                                                                                                                                                    cell line. Codon optimisation results in improved expression of the
                                                             The present sequence is a gag coding region of codon optimised BIV gagpol sequence. This sequence is used in the packaging
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The packaging cell lines and viral particles can be used for gene
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                                                                                                                                                                                                                                                                          71.7%; Score 1059.8; DB 83.6%; Pred. No. 5e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 1257; Conservative
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Best Local Similarity
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